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Pred. No. is the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. 000 W N 156.8 147.2 146.2 146.2 Score 106.8 106.8 92.4 92.4 92.4 61.4 51.6 48.8 47 Match 5 170522 180673 5 180673 5 121341 1 1213469 1 171869 1 171869 1 171869 1 171869 1 171869 1 171869 1 171869 1 171869 1 171869 1 171869 1 171869 1 171869 1 171869 1 171869 1 171869 1 171869 1 171869 0 58377 0 124282 0 173546 4 179055 6905 78359 177829 181507 187495 30493 173546 18743 Length DB 0 0 H 0 N 0 N N N N 0 AC107219 AX148176 AX385037 AX451566 AX385037 AX451562 AX451627 AF453828 AF403384 AC122462 AC121415 AC098607 AC122462 AX385045 AC098607 AX385045 AC098607 AX385045 AC098607 AX385045 AC138708 AC077689 AC121029 AL138708 AC077689 AC021029 AL136106 AC121029 AL13626 AC004157 AC026394 AF030694 AF030693 AF030693 AF030693 AF030693 AC026887 AC0268887 AC0268887 AC0268887 AC0268887 AC008380 AP190500 Homo sapi AC107219 Homo sapi AC148176 Sequence AX385037 Sequence AX385037 Sequence AX451566 Sequence AX451562 Sequence AX451562 Sequence AX451562 Sequence AX451562 Sequence AX451562 Rattus no AC121415 Rattus no AC098607 Rattus no AC122462 Mus muscu AX384516 Sequence AF385047 Sequence AF346501 Mus muscu AX147820 Sequence AF346501 Mus muscu AX147820 Sequence AF138708 Human DNA AC068627 Mus Muscu AC077689 Mus Muscu AC077689 Mus Muscu AC077689 Mattus no AL136106 Homo sapi AC121029 Rattus no AC121029 Rattus no AC121029 Rattus no AC1354453 Sequence AC005504 Plasmodiu AC007157 Plasmodiu AC04157 Plasmodiu AC04157 Plasmodiu AC041591 Homo sapi AC121931 Homo sapi AC1259068 Homo sapi AF09693 Homo sapi AX088165 Sequence AX128507 Sequence Description

ALIGNMENTS

JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AX088165	RESULT 1
Patent: WO 0114548-A 1 01-MAR-2001;	New g-protein coupled receptor and dna sequences thereof	Duecker, K.	1 (bases 1 to 474)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo	Homo sapiens	human.		AX088165.1 GI:13397078	AX088165	ω.	AX088165 474 bp DNA linear PAT 17-MAR-2001		

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REFERENCE
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Vogeli G., Wood, L.S. and Merchant, K. 6 protein-coupled receptors expressed Patent: WO 0131014-A 15 03-MAY-2001; PHARMACIA & UPJOHN COMPANY (US)
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VKKEMILAKRFFFIVFTDALCWIPIFVAKPLSLLQVEIPGTITSWVVIGYSAINSALN
PILYTLTTRPFKEMIIRFWHNYRQRKSMDSKGIRKHMLHHSSGGKCGHCRRCHLS"
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           Homo sapiens.

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2774)

Hsu (S.Y., Kudo, M., Chen, T., Nakabayashi, K., Bhalla, A., van der Spek, P.J., van Duin, M. and Hsueh, A.J.

Spek, P.J., van Duin, M. and Hsueh, A.J.

The three subfamilies of leucine-rich repeat-containing G protein-coupled receptors (LGR); identification of LGR6 and LGR7 and the signaling mechanism for LGR7

Mol. Endocrinol. 14 (8), 1257-1271 (2000)
                                                                                                                                                                                                                                                                         AF190500 2274 bp mRNA Homo sapiens leucine-rich repeat-containing receptor 7 (LGR7) mRNA, complete cds.
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AF190500.1
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WYNYRQRKSMDSKGQKTYAPSFIWVEMWPLQEMPPELMKPDLFTYPCEMSLISQSTRL
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                               CATCATTCATCTGGGGGAAATGTGGCCACTGCAGGAGATGCCACCTGAGTTAA 474
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CATCATTCATCTGGGTGGAAATGTGGCCACTGCAGGAGATGCCACCTGAGTTAA 2197
                                                                                                  TGGCATAACTACAGACAAAGAAATCTATGGACAGCAAAGGTATCAGAAAACATATGCTC
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                                                                           TTGAACCCAATTCTCTATACTCTGACCACAAGACCATTTAAAGAAATGATTCATCGGTTT
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Direct Submission
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EKYICIYVPFRCVFAFFKGTNLAAFIIIVFSYGSMFYSVHQSAITATEIINQVKKEM
ILAKREFFIUFTDALCWIFF IFVVKFLSLLQVEIPGTTTSWVVIFTLATEIINQVKKEM
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/db_xref="taxon:9606"
|. .2274
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                                                                                     Direct Submission
Submitted (27-MAR-2002) Department of Genetics,
Submitted (27-MAR-2002) Department of Genetics,
University, 4444 Forest Park Avenue, St. Louis,
On Mar 16, 2002 this sequence version replaced (
                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (21-FEB-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Direct Submission
Submitted (16-JAN-2002) Genome
Submitted (26-JAN-2002) Genome
                                                                                                                                                                                     Waterston, R.
                                                                                                                                                                                                 MO 63108, USA
6 (bases 1 to 187431)
                                                                                                                                                                                                                                Submitted (16-MAR-2002) Genome University School of Medicine,
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5 (bases 1 to 187431)
Waterston, R.H.
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Isak,A., Meyer,R. and Boyer,E
The sequence of Homo sapiens
Unpublished (2001)
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Genome Res. 8 (11), 1097-1108 (1998)
99063792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 187431)
Sulston, J.E. and Waterston, R.
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Homo sapiens BAC clone RP11-575B4 from 4,
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               Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1
Center project name: H_NH0575B04
                                                                  Center: Washington University Genome Center code: WUGSC
                                               Web site: http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                              Louis,
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., bhred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapphing information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St.
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc Louis

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SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is CTD-2005A22; the clone sequenced to the right is RP11-65M18. Actual start of this clone is at base position 1 of RP11-575B4; actual end is at base position 187431 of
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829. ..938
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                                TCCTTGCCAAACGTTTTTTCTTTATAGTATTTACTGATGCATTATGCTGGATACCCATTT
                                                                                             GTGTTCATCAAAGTGCCATAACAGCAACTGAAATACGGAATCAAGTTAAAAAAAGAGATGA 148
                                                                                                                                                          TTGGTATTAATTTGGCCGCATTTATCATCATAGTTTTTTCCTATGGAAGCATGTTTTATA
                  TCCTTGCCAAACGTTTTTTCTTTATAGTATTTACTGATGCATTATGCTGGATACCCATTT
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/note="similar to !

(NID:g16401965)"
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9126. .9148
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9681. .9926
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/note="similar to Mus musculus
(NID:g16401965)"
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18298. .18349
/rpt_family="Alu"
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2443. 1277
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17849. .18074
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16789. .17233
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7610. .18078
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Pred. No. 7.2e-42;
0; Mismatches 5;
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Sequence 102054.

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        Paszty, C.J., Gong, J., Daugherty, B. and Rogers, N. Leucine-rich repeat-containing g-protein coupled
                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                     Sequence 11 from Patent AX385037
  molecules
                                                                                                                       AX385037.1
                                                                                                                                                                AX385037
                                                                                Homo sapiens
                                                                                               human.
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Mammalia; Butheria; Primates; Cata:
1 (Dases 1 to 1068)
Chen,R., Dang,H.T. and Lowitz,K.P.
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Sequence 17 from Patent
AX148176
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Arena Pharmaceuticals, Inc. (US)
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Sequence 5 f
AX451566
AX451566.1
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Amgen, I
Feder, J.N., Mintier, G., Ramanathan, C.S. and Hawken, D.R. A novel human g-protein coupled receptor, hgprbmy5, exphighly in brain and ovarian tissues Patent: WO 0226824-A 5 04-APR-2002;
                                                                                                                    Homo sapiens
Eukaryota; M
                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; |
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                          human.
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SSPEDDLANNILRIFWWVIRFITCFGNLFVLGMRSFIKAENTTHAMSIKILCCADCLM
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/db_xref="taxon:9606"
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/db_xref="GI:19578161"
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Pred. No. 6.4e-30;
0; Mismatches 117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCTGCTGGATTCCTGTATTTGTAGTTAAAATCCTTTTCCCTCTTCCGGGTGGAAATACCA 1881
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AX385032
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                 Paszty,C.J., Gong,J., Daugherty,B. and Rogers,N. Leucine-rich repeat-containing g-protein coupled molecules and uses thereof patent: WO 0214489-A 6 21-FEB-2002;
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DIKYRGQYQKXALLMMESVQCRLMGFILAMLSTEVSVLLLTYLTLEKFLVIVFPFSNIR
PGKRQTYSVILICIWMAGFLIAVIFFWNKDYFGNFYGKNGVCFPLYYDQTEDIGSKGYS
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/db_xref="taxon:9606"
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Pred. No. 6.3e-30;
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CAAGTTAAAAAAGAGATGATCCTTGCCAAACGTTTTTTCTTTATAGTATTTACTGATGCA
                                                                                           TATTICTCTTGGAATTTTCCTAGGTGTGAACTTGCTGGCTTTTCTCATCATTGTGTTTTCC 1773
                                                                                                         TATTCAGTGGCAATTTTTCTTGGTAITAATTIGGCCGCATTTATCATAAGTTTTTTCC
                                TATATTACTATGTTCTGTTCCATTCAAAAAACCGCCTTGCAGACCACAGAAGTAAGGAAT
                                                         TATGGAAGCATGTTTTATAGTGTTCATCAAAGTGCCATAACAGCAACTGAAATACGGAAT 129
                                                                                                                                                        242;
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Sequence 1 from Patent WO0226824.
AX451562
                                                                                                                                                                                                                                                                                             Feder,J.N., Mintier,G., Ramanathan,C.S. ar
A novel human g-protein coupled receptor,
highly in brain and ovarian tissues
Patent: WO 0226624-A 1 04-APR-2002;
Bristol-Myers Squibb Company (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia;
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ICWIFVFVVKILSLFRVBIPDMYTSWIVIFFLFVNSALNPILYTLTTNFFKDKLKQLL
HKHQRKSIFKIKKKSLSTSIVWIEDSSSLKLGVLNKITLGDSIMKPVS"
1...108
                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
_457 c 416 g 70
                                                                                                                                                                                                                                                                                                                                                                                                       ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 6.3e-30;
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                                                                                                                                                          Score 171.8; DB 6; Pred. No. 6.3e-30; 0; Mismatches 117;
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Best Local Similarity
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                                                                                                                                                      10 TATTCAGTGGCAATTTTTCTTGGTATTAATTTGGCCGCATTTATCATCATAGTTTTTTCC 69
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                                                                                                                         TATTCTCTTGGAATTTTCCTAGGTGTGAACTTGCTGGCTTTTCTCATCATTGTGTTTTTCC 1824
                                                                           TATGGAAGCATGTTTTATAGTGTTCATCAAAGTGCCATAACAGCAACTGAAATACGGAAT
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                                       TATATTACTATGTTCTGTTCCATTCAAAAAACCGCCTTGCAGACCACAGAAGTAAGGAAT 1884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCCTCTATACTCTCACAACCAACTTTTTTAAGGACAAGTTGAAACAGCTGCTGCACAA 2072
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                                                                                                                                                                                                                  242;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1 from Patent WO0214489
AX385027
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Mammalia; Eutheria;
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TQECFLKQYFQCCDCKETELECVNGDLKSVFWLSNNVTLLSLKKKHSLPDKVFIKY
TKLKKIFLQHMCIRHLSRXAFFGLCULQILVLKHNCITTLRGIFKDLHQLTWLLDL
NPITRISQRLFTGLNSLFFLSWVNNYLEALPKOMCAQMFQLNWVDLEGNRIKYLTNST
FLSCDSLTVLFLPRNQIGFVPEKTFSSLKNLGBLDLSSNTIFELSPHLFKDKLLQKL
NLSSNDLMYLHKNQFESLKQLQSLDLERIEIFNJINTRMFQPMKNLSHIFKNERYCSY
APHVRICMFLTIGGISSFEDLLANNILRIFVWVLAFITCFGNLFVIGNRSFIKAENTTH
AMSIKLLCCADCLMGYVLFFVGIFDIKYRGQYGKYALLWMESYGCRMGFLANLSTEV
AMSIKLLCCADCLMGYVLFFVGIFDIKYRGQYGKYALLWMESYGCRMGFLANLSTEV
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YGKNGVCFFLYYDQTEDIGSKGYSLGIFLGVNLLAFLIIVFSYITMFCSIQKTALQTT
EVRNCFGREVAVANREFFIVFSDAICWIPVFVVKILSLFRVEIPDTWTSWIVIFFLPV
                                                                                                                                                                                                                                                                                                                                                              NSALNPILYTLTTNFFKDKLKQLLHKHQRKSIFKIKKKSLSTSIVMIEDSSSLKLGVL
NKITLGDSIMKPVS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (30-NOV-2001) Ob/Gyn, Baylor College
Fannin St., Su. 861, Houston, TX 77030, USA
Location/Qualifiers
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2436 bp
Homo sapiens G protein-coupled rece
decent (GREAT) mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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                    703
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                                                         YGKNGVCFÞLYYDQTEDIGSKGYSLGI FLGVNLLAFLI I VFSY I TMFCSI QKTALQTT
EVRNCFGREVAVANR FFFI VFSDAI CWI PVFVVKI LSLFRVEI PDTMTSWI VI FFLÞV
NSALMPI LYTLTTNFFKDKLKQLLHKHQRKS I FKI KKKSLSTS I VWI EDSSSLKLGVL
                                                                                                                        APHVRICMPLTDGISSFEDLLANNILRIFVMVIAFITCEGNLFVIGMRSFIKAENTTH
AMSIKILCCADCLMGVYLFFVGIFDIKYRGQYQKYALLMMESVQCRLMGFLAMLSTEV
SVLLLTYLTLEKFLVIVFPFSNIRPGKRQTSVILICIMMAGFLIAVIFFMNKDYFGNF
                  NKITLGDSIMKPVS"
503 c 45
                                                                                                                                                                                      TKLKKI FLOHNCIRHI SRKAFFGLCNLQI LYLNHNCI TTLRPGI FKDLHQLTWLI IDD
NPI TRI SQRJFTGLNSLF FLSMYNNY LEALF KOMCAQMPQLLNWDLEGKRI KXLTNST
FLSCOSLTVLFLPRNQI GFV PEKTFSSLKNLGELDLSSNTI TBLSPHLFXDLKLLQKL
LLSSNPLMYLHKNQFESLKQLQSLDLER I E I PN I NTRMFQPMKNLSHI Y FKNFRY CSY
                                                                                                                                                                                                                                                                               /translation="mivflvfkhlfslrlitmffllhfivlinvkdfaltogsmitps
CQKGYFPCGNLTKCLPRAFHCDGKDDCGNGADEENCGDTSGWATIFGTVHGNANSVAL
TQECFLKQYPQCCDCKETELECVNGDLKSVPMISNNVTLLSLKKNKIHSLPDKVFIKY
                                                                                                                                                                                                                                                                                                                                                                                          descent"
                                                                                                                                                                                                                                                                                                                                             /protein_id="AAL73946.1"
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                                                                                                                                                                                                                                                                                                                                                                                                            /product="G protein-coupled receptor affecting testicular
                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="GREAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /map="13q12-q13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="GREAT"
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Query Match 36.2%; Best Local Similarity 67.4%; Matches 242; Conservative

Score 171.8; DB 9; Pred. No. 6.2e-30; 0; Mismatches 117;

Length Indels

Gaps

0

2436;

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BASE CO

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COMMENT
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REFERENCE
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AUTHORS
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ORGANISM
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AF403384
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                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTCTCTATACTCTGACCACAAGACCATTTAAAGAAATGATTCATCGGTTTTTGGCATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTACCATAACCTCTTGGGTAGIGATTGGTTATTCTGCCATTAACAGTGCTTTTGAACCCA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCTGCTGGATTCCTGTATTTGTAGTTAAAATCCTTTCCCTCTTCCGGGTGGAAATACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTATGCTGGATACCCATTTTTGTAGCGAAACCTCTTTCACTGCTTCAGGTAGAAATACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATATTACTATGTTCTGTTCCATTCAAAAAACCGCCTTGCAGAACCACAGAAGTAAGGAAT 1954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACACAATGACTTCCTGGATAGTGATTTTTTTCCTTCCAGTTAACAGTGCTTTGAATCCA
                                                                                                                                                                                                                                               Sequence update by submitter
On Feb 19, 2002 this sequence version
Cocation/Qualifiers
1. . 2838
                                                                                                                                                                                                                                                                                                                                              Submitted (19-FEB-2002) Division of Reproductive Biology, Department of Gynecology and Obstetrics, Stanford University Medical Center, 300 Pasteur Drive, Room A-344, Stanford, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sherwood,O.D. and Hsueh,A.J. Activation of orphan receptors by the hormone relaxin Science 295 (5555), 671-674 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens LGR8 mRNA, AF403384
                                                                                                                                                                                                                                                                                                                           94305-5317, USA
                                                                                                                                                                                                                                                                                                                                                                                                                        Hsueh, A.J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stanford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (26-JUL-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hsu, S.Y., Nakabayashi, K. and Bhalla, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hsu, S.Y., Nakabayashi, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
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              /protein_id="AAL69324.2"
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/db xxef="G1:18702460"
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TQBCFLKQYFQCCDCKETELECVNGDLKSVFMISNNVTLLSLKKNKIHBLFDKVFIKY
                                                                                                                                                      107
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CA 94305,
TKLKKI FLQHNCI RHI SRKAFFGLCNLQI LYLNHNCI TTLRPGI FKDLHQLTWLI LDD
                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                            product="LGR8"
                                                                                                                              codon_start=1
                                                                                                                                                                map="11q13"
                                                                                                                                                                                         chromosome="11"
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                                                                                                                                                                                                                                                                                     gi:18419431
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KEYWORDS
SOURCE
ORGANISM
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VERSION
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AC128964
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Best Local Similarity
Matches 242; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
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Rattus

Rattus

(bases 1 to 58377)

RS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Farnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
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Mammalia; Eutheria;
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ABHYRICKPLTOGISSFEDLLANNILRIFYND INTRMFQPKKNLSHIYFKNERYCSY
APHYRICKPLTOGISSFEDLLANNILRIFYND INTRMFQPKNLSHIYFKAENTTH
AMSIKILCKADCLMGVYLLFFVGIFDIKYRGQXCKYALLMMESVQCRLMGFLAMLSTEV
SVLLLTYLTLEKFLVIVFPSNIRPGKRQTSVILICIWAAGFLIAVIFFWNKDYFGNF
YGKNGVGFPLYVDQTEDIGSKGYSLGIFLGVNLLAFLIIVFSVITMFCSIQKTALQTT
EVRNCFGREVAVANRFFFIVFSDAICMIPVFVKKILSLFRVEIPDTMTSWIVIFFLEV
NSALNFILYTLTNWFFKDKLKQLLHKHQRKSIFKIKKKSLSTSIVWIEDSSSLKLGVL
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Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlsson, E., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.C., Li, J., Li, J., Li, Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.C., Li, J., Li, J., Li, J., Liu, M., Loulseged, H., Lozado, R. J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Mahsshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Ngyen, N., Ngyen, N., Moser, M., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Petery, J., Peters, L., Pickens, R., Primus, B., Py, L.L., Quiles, M., Ren, Y., Peters, L., Pickens, R., Primus, B., Py, L.L., Quiles, M., Ren, Y., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, B., Sonaike, T., Sparks, A., Stanley, H., Stome, H., Sutton, A., Svatek, A., Tamerisa, A., Tamerisa, K., Tang, H., Tamey, J., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Umang, S., Ward-Moore, S., Warren, R., Washington, C., Watliamson, R., Wang, Q., Wullamson, S., Wulliamson, A., Wulczyk, R., Woden, S., Watliamson, R., Wang, Q., Wulce, M., Y., Y., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                         NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).

NOTE: This is a "working draft" sequence. It currently consists of 36 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 20312 bases at least Q40
Consensus quality: 22274 bases at least Q30
Consensus quality: 23493 bases at least Q20
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Center clone name: CH230-179I5
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Unpublished

JOURNAL

Direct Submission 2 (bases 1 to 58377) Worley, K.C.

COMMENT

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On Jul 18, 20
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Baylor Plaza, Houston,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 52 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jul 18, 2002 this sequence version replaced gi:20976361
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Center clone name: CH230-39G4
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Center clone name: CH230-39G4
Center plasmid;
Chemistry: Dye-terminator Big Dye:
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Pred. No. 6.8e-30; 0; Mismatches 44

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***, 66 unordered pieces.
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Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;

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Direct Submission
Direct Submission
Submitted (26-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 173546)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (12-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 11, 2002 this sequence version replaced gi:17973780.

Center: Baylor College of Medicine Center code: BCM,
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Direct Submission
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NOTE: This is a 'working draft' sequence. It currently consists of 66 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Center project name: GILC
Center clone name: CH230-148B15
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
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                                                  AAF28059
AAI99557
ABK43573
AAD06507
AAZ90524
AAZ25345
AAZ25346
AAI99584
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                                                                       (without alignments)
4723.218 Million cell updates/sec
Human HGRL101 G-pr
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DNA encoding novel
Human CN222 G pro
Human GPCR pxotein
Human LGR7 long fo
Human LGR7 short f
Human LGR7 short f
Human musculoskele
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	AAX83936	20	24701	8.1	38.4	44	
	AAX83935	20	24701	8.1	38.4	43	ი
	AAX83944	20	8967	8.1	38.4	42	
	AAX83942	20	8967	8.1	38.4	41	ი
	AAX83940	20	8967		38.4	40	
	AAX83938	20	8967	8.1	38.4	39	ი
nella t	AAX83965	20	1797	8.1	38.4	38	ი
immune syst	ABL33629	24	12138	8.2	38.8	37	
Human chemically p	ABK40034	24	12138	8.2	38.8	36	
Drosophila melanog	ABL15482	23	39536	8.3	39.4	35	
Human immune syste	ABL34174	24	113515		٠	34	
BAC containing rep	AAF22286	21	134499	8.5	40.2	ω u	a
	ABK83490	24	5644	•	44	32	
Human breast and o	AAF21792	21	4292	9.3	44	32	
	ABL07293	23	1015	10.3	48.8	30	
cDNA encoding Dros	AAS57085	22	2	10.3	48.8	29	
Human nGPCR57 codi	AAH51001	22	1018	22.5	106.8	28	a
	AAA44932	21	636	32.6	154.4	27	
	AAD32027	24	321	33.1	156.8	26	
	ABL40196	24	2262	•	171.8	25	
enc	ABK51944	24	2214	36.2	171.8	24	
n G prote:	ABL40197	24	2190		٠	23	
enc	ABK51947	24	2142		171.8	22	
വ	ABL40188	24	1830	36.2		21	
Ω	ABL40191	24	1545		٠	20	
	ABL40192	24	1473			19	
6	AAS07943	22	1068		•	18	
Human G protein-co	ABL40194	24	1065		171.8	17	
Human ORFX ORF1290	AAC75735	21	420	•	353.2	91	
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Human cDNA SEO ID	ABA06471	22	530	92.6	38.	10	
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ALIGNMENTS

Human; HGRL101; G-protein coupled receptor; infection; pain; cancer; diabetes; obesity; eating disorder; asthma; Parkinson's disease; hypotension; osteoporosis; myocardial infarction; migraine; allergy; psychotic disorder; neurological disorder; dyskinesia; vaccine; ss. Human HGRL101 G-protein coupled receptor coding sequence WO200114548-A2 Homo sapiens. AAF28059; AAF28059 standard; cDNA; 474 BP 23-MAY-2001 (first entry /*tag= a /product= "HGRL101" /partial Location/Qualifiers

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Best Local Simi
Matches 474;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel G-coupled protein receptor, HGRL101 useful for treating diseases such as microbial infections, cancers, obesity, asthma, diabetes, hypotension, osteoporosis, myocardial infarction, stroke, ulcer, allergy -
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P-PSDB; AAB35407.
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Human; nootropic; neuroprotective; cytostatic; dermatological; viruci immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnera antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human expressed polynucleotide SEQ
                                                                                                                                                                                                                                                                                                                                                       virucide,
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ID NO 20

02-AUG-2001. WO200155387-A1

30-JUN-2000;
30-JUN-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
14-JUG-2000;
16-JUG-2000;
16-JUG-2000;
17-JUG-2000;
18-JUG-2000;
19-JUG-2000;
19-JU 24-FEB-2000; 02-MAR-2000; 16-MAR-2000; 17-MAR-2000; 18-APR-2000; 19-MAY-2000; 07-JUN-2000; 17-JAN-2001; 2000US-0184664. 2000US-0186350. 2000US-0189874. 2000US-0190076. 2000US-0198123. 2000US-0205515. 2000US-0225266 2000US-0225268 2000US-0225268 2000US-0225270 2000US-0225477 2000US-0225757 2000US-0225758 2000US-0225758 2000US-0225759 2000US-0226279 2000US-0226681 2000US-0216880. 2000US-0217487. 2000US-0217496. 2000US-0214886. 2000US-0215135. 2000US-0216647. 2000US-0229924 2000US-0229343 2000US-0229344 2000US-0229344 2000US-0229345 2000US-0229509 2000US-0229509 2000US-0239513 2000US-0231242 2000US-0231242 2000US-0231244 2000US-0231244 2000US-0231244 2000US-0231244 2000US-0231249 2000US-0231249 2000US-0231249 2000US-0231249 2000US-0231298 2000US-0231298 2000US-0232981 2000US-0232981 2000US-0232981 2000US-0232981 2000US-0226868. 2000US-0227182. 2000US-0227009. 2000US-0224518. 2000US-0224519. 2000US-0225213. 2000US-0225214. 2000US-0218290. 2000US-0220963. 2000US-0220964. 2001WO-US01310 2000US-0209467

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CC objects The sequence data for this patent did not form part of the corm will only at fitp. wipo.int/pub/published_pct_sequences.
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Matches 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1089
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                  TTGAACCCAATTCTCTATACTCTGACCACAAGACCATTTAAAGAAATGATTCATCGGTTT
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                                                              GAAATACCAGGTACCATAACCTCTTGGGTAGTGATTTTTATTCTGCCCATTAACAGTGCT
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   2000US-0186350.
2000US-019874.
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2000US-0216486.
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                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is also useful for identifying compounds useful for treating other schizophrenia. These compounds are also useful for treating other neurological and psychiatric diseases, e.g. (depression, anxiety, bipolar disease, affective disorders, attention deficit hyperactivity disorder/attention deficit disorder, epilepsy, neuritis, neurasthenia, neuropathy, neurosis, Alzheimer's disease, Parkinson's disease, migraine and senile dementia. The invention also provides genetic screening procedures that entail analysing a person's genome with respect to GPCR. The vectors are useful for the recombinant production of the GPCR's. The present DNA sequence encodes human CON222 G protein-coupled receptor (GPCR) protein.
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(first
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                                                               CDNA; 1804
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Pred. No. 3.5e-109;
                                                               ВP
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention provides human G protein coupled protein receptor (HGPRP) polypeptides and polymucleotides encoding them. The polypeptides can be produced by standard recombinant methodology. The polymucleotides and polypeptides may be used in the prevention, treatment and diagnosis of diseases associated with their inappropriate expression. Diseases that can be treated are cell proliferative disorders (e.g. arteriosclerosis, atherosclerosis and hepatitis), cancers (e.g. leukemia, melanomas and adenocarcinoma), immune disorders (e.g. anemia, asrhma and Crohn's disease) and neurological disorders (e.g. epilepsy, Alzheimer's disease and Barkinson's disease). The anti-hGPCR antibodies may also be used as diagnostic agents for detecting the presence of HGPRP polypeptides in samples (e.g. by persyme linked immunosorbant assay (ELISA)). Sequences ARZ90521-526 represent CDNA fragments encoding the HGPRP polypeptides in the presence of the presence of the procession of the proces
  1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bandman O,
Baughn MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1804 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; Page 69-70; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human G protein coupled protein receptor peptides useful for the prevention, diagnosis and treatment of cell proliferative, neurological
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anti-Alzheimer's; anti-Parkinsonian; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neurological; immune disorder; cytostatic; anti-arteriosclerotic; anti-atherosclerotic; hepatotropic; antiinflammatory; virucide; leu immunomodulatory; anemia; asthma; gastrointestinal; anti-epileptic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INCY-) INCYTE PHARM INC.
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                                241 GAAATACCAGGTACCATAACCTCTTGGGTAGTGATTGGTTATTCTGCCATTAACAGTGCT
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GAAATACCAGGTACCATAACCTCTTGGGTAGTGATTTTTATTCTGCCCATTAACAGTGCT
                                                                                                                          ACTGATGCATTATGCTGGATACCCATTTTTGTAGCGAAACCTCTTTCACTGCTTCAGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lal P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0156513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 439.2;
Pred. No. 4e-1
0; Mismatches
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                                                                                                                  Matches
                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                          The present sequence encodes the human G-protein coupled receptor having extracellular leucine rich repeat regions, designated IGR7 long form. The LGR4, LGR5 and LGR7 proteins are used to identify ligands for the receptor. The polypeptides and/or polynucleotides are also useful for homologous or related genes, producing compositions that modulate the expression or function of the receptors, gene therapy, mapping functional regions of the receptors, studying associated physiological pathways, in vivo prophylactic and therapeutic purposes, as immunogens for producing antibodies, and for identifying biologically active agents. The polypeptides contain a G-protein coupled seven transmembrane region and a leucine rich repeat extracellular domain. These regions capture and facilitate optimal orientation of its ligand.
                                                                                                                                                                                                                Sequence 2467 BP; 747 A; 487 C; 474 G; 759 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New G-protein coupled receptors, useful for identifying their own
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-591074/50
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                                                                                                                                             Similarity
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                                                                                                                  Conservative
                                                                                                                                                                                                                                                                              are also expressed in diverse tissues.
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The present sequence encodes the human G-protein coupled receptor having extracellular leucine rich repeat regions, designated LGR7 short form. The LGR4, LGR5 and LGR7 proteins are used to identify ligands for the receptor. The polypeptides and/or polynucleotides are also useful for homologous or related genes, producing compositions that modulate the expression or function of the receptors, gene therapy, mapping functional regions of the receptors, studying associated physiological
                                                                                                                                                                                                          Claim 4; Fig 4; 54pp;
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extracellular leucine rich repeat region; mapping; identification;
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Isolated digestive system associated polypeptide for treating, preventing and/ or prognosing disorders related to the digestive system
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P-PSDB; AAM99972.
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2000US-0239935.
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including digestive system e.g. diagnosis -
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509pp + Sequence
                                             cancers and also for testing and detection
    Listing;
    English
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cc (AAM99936-AAM99984) useful for preventing, treating or ameliorating cc (AAM99936-AAM99984) useful for preventing, treating or ameliorating cc medical conditions e.g. by protein or gene therapy. The genes are cc isolated from a range of human tissues disclosed in the specification. CC The nucleic acids, proteins, antibodies and (ant) agonists are useful cc in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast cc and ovarian cancer and other cancers of the adrenal gland, bone, bone cc marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune cc disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (c) wound healing; (e) neurological diseases e.g. cerebral anoxia and cc epilepsy; and (f) infections diseases such as viral, bacterial, fungal cc Note: The sequence data for this continual contents of the sequence data for this contents. The sequence data for this patent did not form part of ted specification, but was obtained in electronic format WIPO at ftp.wipo.int/pub/published_pct_sequences. format directly

158 A; 105 C; 95 G; 171 T; 1 other;

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1 GCCCAGATTTAITCAGTGGCAATTTITCTTGGTAITAATTTGGCCGCATTTATCATCATA
                                                                                                                                                                                                          GAAATACCAGGTACCATAACCTCTTGGGTAGTGATTGGTTATTCTGCCATTAACAGTGCT
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CATCATTCATCTGGGGGGAAATGTGGGCCACTGCAGGAGATGCCACCTGAGTTAA 474
                                                                                                                                TTGAACCCAATTCTCTATACTCTGACCACAAGACCATTTAAAGAAATGATTCATCGGTTT
                                           TGGTATAACTACAGACAAAGAAATCTATGGACAGCAWAGG--TCAGAAAACATATGCTC
                                                                     TGGCATAACTACAGACAAAGAAATCTATGGACAGAAGGTATCAGAAAAACATATGCTC
                                                                                                               TTGAACCCAATTCTCTATACTCTGACCACAAGACCATTTAAAGAAATGATTCATCGGTTT
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96.6%;
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Pred. No. 3.5e
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AAL35644 standard; (first entry) CDNA; 530 ВP

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Human musculoskeletal system related polynucleotide SEQ ID NO 986

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2000US-0233063.	2000US-0232401.	2000US-0232400.	2000US-0232398.	200005-0232397.	2000US-0231968.	200005-0232080.	200005-0231414.	2000US-0231413.	2000US-0231244.	2000US-0231243.	2000US-0231242.	2000US-0230438.	2000US-0230437.	2000US-0229513.	2000US-0229509.	2000US-0229345.	200005-0229344.	200103-0202343.	200005-0229287.	2000105-0220504.	200005-0227009.	2000US-022/182.	200000 - 00000000.	2000005-0226681.	200018-0226279.	2000008-0225/59.	200008-0225758.	000000-00001017	300010 - 003011111111 - 0030111111111111	2000118-0225A47	2000115-0225270	200005-0225268	2000US-0225267.	2000US-0225266.	2000US-0225214.	2000US-0225213.	2000US-0224519.	2000US-0224518.	2000US-0220964	200003-0220963	2000105-0218-200	200015-0217406 200015-0217406	200015-0212000:	300016-0216647.	200008-0215135.	200008-0214886.	200008-0209467.	2000US-0205515.	2000US-0198123.	2000US-0190076.	2000US-0189874	2000US-0186350.	200015-010045A	200015-01/9003.		2001WO-US01338.				A1.			n; 88.	infection; human; secreted protein;	omic; ancibacterial; antifungal; antiparasitic	hepatotropic; antidiabetic; antiinflammatory; antiulce	umunosuppressive; nootropic; neuroprotective;	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis, 
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08-DEC-2000;
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05-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           parasitic infections.

Note: The sequence data for this patent did not form printed specification, but was obtained in electronic printed specification, but was obtained pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g. diagnosis -
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                       TGGCATAACTACAGACAAAGAAAATCTATGGACAGCAAAGGTATCAGAAAACATATGCTC
                                                                                                          TTGAACCCAATTCTCTATACTCTGACCACAAGACCATTTAAAGAAATGATTCATCGGTTT
                                                                                                                                                                       GAAATACCAGTACCATAACCTCTTGGGTAGTGATTTTTATTCTGCCCATTAACAGTGCT
                                                                                                                                                                                                                                                              ACTGATGCATTATGCTGGATACCCATTTTGTAGCGAAACCTCTTTCACTGCTTCAGGTA
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TGGTATAACTACAGACAAAGAAATCTATGGACAGCAWAGG-
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Pred. No. 3.5e
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14-JUG-2000;
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04-FEB-2000;
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2000US-198230P.
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2000US-219886P.
2000US-216487P.
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2000US-217496P.
2000US-217496P.
2000US-229964P.
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01-DEC-2000;
05-DEC-2000;
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05-DEC-2000;
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06-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                        The present invention provides human cDNAs, proteins and related 9 DNAs. These can be used in the treatment of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascula renal and proliferative disorders and inflammation. The present se is a cDNA of the invention.
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P-PSDB;
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DB; ABB10249.
                                                                                                                         ACTGATGCATTATGCTGGATACCCATTTTTGTAGCGAAACCTCTTTCACTGCTTCAGGTA
                                                                                                                                                                               ATACGGAATCAAGTTAAAAAAGAGATGATCCTTGCCAAACGTTTTTTCTTTATAGTATTT
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           TGGCATAACTACAGACAAAGAAAATCTATGGACAGCAAAGGTATCAGAAAACATATGCTC
                                                  TTGAACCCAATTCTCTATACTCTGACCACAAGACCATTTAAAGAAATGATTCATCGGTTT
                                                                                  GAAATACCAGGTACCATAACCTCTTGGGTAGTGATTTTTATTCTGCCCATTAACAGTGCT
                                                                                              GAAATACCAGGTACCATAACCTCTTGGGTAGTGATTGGTTATTCTGCCATTAACAGTGCT
                                                                                                                                                                    TGGTATAACTACAGACAAAGAAATCTATGGACAGCAWAGG-
                                        TTGAACCCAATTCTCTATACTCTGACCACAAGACCATTTAAAGAAATGATTCATCGGTTT
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2000US-251030P.

2000US-251130P.

2000US-251479P.

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                                                                                                                                                                                                                                                                                                          Score 438.8;
Pred. No. 3.5
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27-SEP-2000
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2000US-231242P.
2000US-231243P.
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2000US-231968P.
2000US-23239P.
2000US-23239P.
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2000US-23239P.
2000US-233364P.
2000US-233365P.
2000US-23493P.
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2000US-23463P.
2000US-24463P.
2000US-244647P.
2000US-24661P.

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RESULT 11
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ID AAS28
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XX CDNA
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07-JUN-2000

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2000US-0229467

2000US-0214886

2000US-0215135

2000US-0215136

2000US-0217487

2000US-0217487

2000US-0217496

2000US-022963

2000US-0224519

2000US-0224519

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2000US-0225214

2000US-0225266

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2000US-0225267

2000US-0225757

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2000US-0225344

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22-CCT-2000

23-SEP-2000

23-SEP-2000

24-CCT-2000

25-SEP-2000

26-CCT-2000

27-SEP-2000

28-NOV-2000

29-SEP-2000

20-CCT-2000

20-CC
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2000US-0231413.
2000US-023298.
2000US-0232398.
2000US-0232399.
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                                                                                                                                                                                                                                                                                                                                atches 458;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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11-DEC-2000;
05-JAN-2001;
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                                                                                                                         ACTGATGCATTATGCTGGATACCCATTTTGTAGCGAAACCTCTTTCACTGCTTCAGGTA
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               TTGAACCCAATTCTCTATACTCTGACCACAAGACCATTTAAAGAAATGATTCATCGGTTT
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2000US-0250160.
2000US-0250391.
2000US-0251988.
2000US-0256719.
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Pred. No. 3.5e-109;
1; Mismatches 13;
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14-BUG-2000;
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  14-AUG-2000;
22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
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28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
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19-MAY-2000;
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17-MAR-2000;
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  2000US-0220963.

2000US-02295419.

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2000US-0225213.

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                                                                                                                                             CC Sequences AAS29511-AAS29736 represent cDNA molecules, which encode the CC endocrine polypeptides of the invention. Endocrine polypeptides and their CC associated polymucleotides of the invention are useful in the diagnosis, CC treatment and prevention of various types of disorders in e.g. humans, CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A CC pathological condition can be determined by determining the presence or a mutation in an endocrine polymucleotide. The treatable CC disorders include autoimmune diseases such as rheumatoid arthritis, CC hyperproliferative disorders such as neoplasms of the breast or liver, CC cardiovascular disorders such as cardiac arrest, cerebrovascular CC disorders such as cerebral ischaemia, nervous system disorders such as Albeimer's disease, infections caused by bacteria, viruses and fungi, CC coular disorders such as corneal infection, endocrine disorders such as CC crohn's disease, renal disorders such as glomerulonephritis and CC crohn's disease, renal disorders such as glomerulonephritis and CC cromature labour and infertility, gastrointestinal disorders such as CC crohn's disease, renal disorders such as glomerulonephritis and CC cromature disorders such as asthma. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sumburn, to maintain CC mass before transplantation, to regenerate tissues and in chemotaxis. The polypeptides can also be used to aid corders such as storage capabilities.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                      Query Match
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Matches 458;
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P-PSDB;
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Similarity 96.6%;
58; Conservative
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23-AUG-2000 21-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 06-SEP-2000 06-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 14-SEP-2000 12-SEP-2000 14-SEP-2000 15-SEP-2000 20-OCT-2000 20-OCT-2000 20-OCT-2000 20-OCT-2000 20-OCT-2000 20-OCT-2000 20-OCT-2000 02-OCT-2000 03-NOV-2000 04-NOV-2000 08-NOV-2000 08-NO

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RESULT 13
AAS30187
ID AAS30
XX AAS30
XX AAS30
XX AAS30
XX DT 21-N0
CXX DNA 6
CXX Human
KW Human
KW cardi
KW cardi
KW blook
KW blook
KW blook
KW blook
31-JAN-2000

04-FEB-2000

24-FEB-2000

02-MAR-2000

16-MAR-2000

17-MAR-2000

18-PR-2000

19-MAY-2000

07-JUN-2000

28-JUN-2000

30-JUN-2000

07-JUL-2000

11-JUL-2000

11-JUL-2000

11-JUL-2000

11-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                autoimmune disease; inflammatory disease; reproductive system disorder; endocrine disorder; neural activity; neurological disorder; wound healing; respiratory disorder; ss.
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   2000US-0179065.

2000US-0184664.

2000US-0184564.

2000US-018350.

2000US-0190076.

2000US-0190076.

2000US-029467.

2000US-0214886.

2000US-0214886.

2000US-02148880.

2000US-0217487.

2000US-0217487.
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26-JUL-2000;
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22-AUG-2000;
23-AUG-2000;
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25-SEP-2000;
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2000US-0220963.

2000US-0220964.

2000US-0224518.

2000US-0224519.

2000US-0225213.

2000US-0225214.

2000US-0225266.

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2000US-0227182

2000US-0227182

2000US-0227009

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2000US-0229344

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2000US-0225270.
2000US-0225447.
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08-NOV-2000
17-NOV-2000
17-NOV
                           diagnosing, treating, preventing and/or prognosing disorders related these polypeptides. The polynucleotides are especially useful in the diagnosis, prognosis, prevention and/or treatment of diseases which include kidney disorders (e.g. renal failure or nephritis), cardiovascular disorders (e.g. hypertension or myocardial infarction) blood disorders (e.g. anaemia or blood coagulation disorders), electrolyte imbalance disorders (e.g. hyponatraemia or hyperkalaemia)
                                                                                                                                                                    The
                                                                                                                                                                                                                                                        New polynucleotides and polypeptides, useful for diagnosing, treating, preventing or prognosing e.g. kidney, cardiovascular, blood, electrolyte imbalance or neoplastic disorders, autoimmune diseases,
                                                                                                                                                                                                         Claim
                     neoplastic
                                                                                                                                                                    invention
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)B; AAU18666.
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disorders (e.g. nephtoma or cancers, inflammatory disease
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2000US-0246475.
2000US-0246477.
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2000US-0251989.
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S-0254097.
S-0259678.
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S-0249300.
S-0250160.
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3-0249208.

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3-0249212.

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                 renal cell cancer)
                                                                                                         d polypeptides useful ing disorders related incecially useful in the of diseases which
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autoimmune

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RESULT 14
AAS34845
ID AAS34
XX AAS34
XX AAS34
XX CDNA
CDT 04-DE
CDNA
XX Human
XW Human
XW hyper
XW muscu
XW muscu
XW muscu
XW muscu
XW muscu
XW Myper
XW MO200
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  31-JAN-2000;
04-FEB-2000;
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                                                                             17-JAN-2001; 2001WO-US01358
                                                                                                                                                                                                                                                                                                    Human; neoplastic disease associated polypeptide; cancer; gene thera hyperproliferative disorder; neural disorder; immune system disorder muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder;
                                                                                                                                                                               WO200155163-A1
                                                                                                                                                                                                                                                                                 neuroprotective;
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                                                                                                                                                                                                                               sapiens
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08-NOV-2000

09-NOV-2000

01-NOV-2000

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17-NO
        Novel polypeptides and polynucleotides useful as diagnostic reagent diagnose diseases or disorders associated with aberrant expression activity of polypeptides, and for treating cancers, rheumatoid arthritis -
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P-PSDB; AAU21646.
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Matches 458
Central nervous system; CNS; hyperproliferative disorder;
                                                       DNA encoding novel central nervous system protein #455.
                                                                                                       05-JUN-2002
                                                                                                                                                                                        ABK43875 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gastrointestinal disorders, pulmonary disorders, cardiovascular disorders and renal disorders. The polynucleotide sequences of the invention are also useful in gene therapy. AAS34767-AAS35505 represent cDNA sequences encoding for the novel human neoplastic disease associated polypeptides
                                                                                                                                                   ABK43875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hyperproliferative disorders (e.g. leukaemia, bone cancer, bladder cancer, brain stem glioma, adult liver cancer, childhood cerebellar astrocytoma, or Hodgkin's lymphoma). The sequences of the invention may also be useful for treating other disorders such as neural disorders, immune system disorders, muscular disorders, reproductive disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to the isolation of novel human neoplastic disease associated polypeptides (AAU21568-AAU21851), and cDNA and DNA sequences encoding for these polypeptides. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or progness of disorders involving neoplastic disease such as
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cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; additive; food preservative; gene therapy; gene; ss.

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17-JAN-2001; 2001WO-US01332 ; 2000US-0179065. ; 2000US-0180628. ; 2000US-0184664. ; 2000US-0186350. ; 2000US-0189874.

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autoimmune disease; rheumatoid arthritis; neoplasm; cardiovascular disorder;

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11-DEC-2000;
05-JAN-2001;
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                                                                TTGAACCCAATTCTCTATACTCTGACCACAAGACCATTTAAAGAAATGATTCATCGGTTT
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Pred. No. 3.5e~:
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BB632910 BB632910 H17265 ym37b10.r1 AQ697633 HS_5525 B AL107199 Drosophil AL440253 T7 end of

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 200000000
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           320.4
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Match
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Gapop 10.0 , Gapext 1.0
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        BQ228832
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BF942735
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BF021857 uy58h08.y
                                                                               Description
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TITLE
JOURNAL
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42.2
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13304 row: m column: 12
High quality sequence start: 87
High quality sequence stop: 603.
Location/Qualifiers
                                                                                                       1 (bases 1 to 841)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 841)
                                                                                                                                                                                                                                                       BQ228832
841 bp mRNA linear EST 02-MAY-200
AGENCOURT_7522585 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6051251
5', mRNA sequence.
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BQ228832.1 GI:20410232
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AQ775943
PB178873
CNS002DA
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CNS0478
PB152955
AC117867
PB152955
AC117868
PG13125
AC179977
PB16535
AC1799689
BH007158
BF033125
AC179689
BH007158
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AL103731 Drosophil
AQ775843 HS 2151 B
BF178875 601807574
AL27030 Tetracdon
AL206466 Tetracdon
AL206466 Tetracdon
AL2064634 Drosophil
AL108811 Drosophil
AL108811 Drosophil
AL108811 Drosophil
AL108811 BOMDB70TR
BH5583030 kj36c08.y
AG03218 Pan trogl
AL25017 Tetracdon
BH681813 BOMDB70TR
BH559463 BOGEW97TF
C91574 C91574 G91574 G91574
BH52955 Gm_UMD001
AL17864 P8730bil
AL17864 P8730bil
AL276226 Tetracdon
AV698306 AV698306
AZ432873 1M0218A01
AL07915 Drosophil
AQ77977 HS 5572
BAZ584622 ENTFUH41TF
BF986555 CM3-GN005
AA128093 zl14e05.r
AW158885 IL2-ENT019
BF032125 601559730
AL108705 Drosophil
AQ739689 PESTCAB4
BH007158 ee63g04.x
AL266908 Tetracdon
AL760324 Arabidops
BF725643 bx17f03.y
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RESULT 2
BG304121/c
LOCUS
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ORIGIN
                                                                                                                                                                      TITLE
JOURNAL
COMMENT
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AUTHORS
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KEYWORDS
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                            BG304121
BG304121.1
EST.
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Sugano,S., Kawakami,K., Johnson,S., Li,F., Marra,M., Eddy,S.,
Hillier,L., Clifton,S., Allen,M., Gibbons,M., Jost,S., Kucaba,T.,
Martin,J., Pape,D., Steptoe,M., Underwood,K., Theising,B., Ritter
,E., Bowers,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU Zebrafish EST Project 1999
Unpublished (1999)
Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution information can be found through the I.M.A.G.E.
                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                          Contact: S.L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                     Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG304121 744 bp mRNF
fl30f05.x1 Sugano Kawakami zebrafish DR
3815552 3' similar to TR:Q9VBP0 Q9VBP0
                                                               Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
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/db xref="taxon:9606"
/clone="IMAGE:6051251"
/clone lib="NIH MGC 72"
/tissue type="melanottc melanoma"
/tissue type="melanottc melanoma"
/lab_host="PH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Syreage insert size 2 kb. Library constructed by Life
Technologies."
Technologies."
170 g 269 t 2 others
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Pred. No. 1.5e-70;
0; Mismatches 16
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DRA Danio rerio cDNA clone
PO CG5042 PROTEIN. ;, mRNA
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by Life
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Best Local Similarity
Matches 215; Conserv
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                                                                                                                                                                                                                                                                                    TGGGTAGTGATTGGTTATTCTGCCATTAACAGTGCTTTGAACCCCAATTCTCTATACTCTG
                                                                                                                                                                                                                                                                                                                       ATATTCATGGTCAAAATCCTCTCTAATGGAGGTGGAGATACCAGGAACCATCACATCT
                                                                                                                                                                                                                                                                                                                                                ATTTTTGTAGCGAAACCTCTTTCACTGCTTCAGGTAGAAATACCAGGTACCATAACCTCT
                                                                                                                                                                                                                                                                                                                                                                                            ATGATCCTTGCCAAACGTTTTTTTTTATAGTATTTACTGATGCATTATGCTGGATACCC
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                                                                                                                                                                                                                   ACCACCAGTTTTTTCAGAGAGCAGGTGGAACATTTATGGGGACACT
                                                                                                                                                                                                                                                                      TGGGTGGTGATCTTCATCCTGCCCATCAACAGTGCCTTAAACCCCATCCTTTACACACTG
                                                               pig.
Sus scrofa
                                                                                            75600 MARC
AW436170
AW436170.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Consortium/LLNL, send emanded primer: T7 from Gibco High quality sequence stop
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 235)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T. Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A.,
                                                                                                                                                  AW436170
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="Sugano Kawakami zebrafish /sex="mixed (one male and one female, unfertilized eggs)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:7955"
/clone="3815552"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     strain="AB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Danio rerio"
                                                                                                                                     2PIG
                                                                                                           GI:6971476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.8%;
                                                                                                                                     Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                send email to: info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 136.4; DB 12; Pred. No. 3.9e-24;
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                                                                                                                                     cDNA
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laequence.
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                   Smith, T.P.L.,
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    .P.L., Casas,E.,
Laegreid,W.W.
                                             Euteleostomi;
Sus.
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BF942735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 TTCCTTCCGGTGAACAGTGCCTTGAACCCAATCCTTTACACTCTCACAACCAGCTTTTTC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 CGTTTTTTCTTTATAGTATTTACTGATGCATTATGCTGGATACCCATTTTTGTAGCGAAA 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAGAAATGATTCATCGGTTTTGGCATAACTA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTCTTTCACTGCTTCAGGTAGAAATACCAGGTACCATAACCTCTTGGGTAGTGATTGGT 279
                                                                                                                                                                                                                                                                                                                                                                                                            AAGGACACGTTGAAACAGCTGCTGCACAACCA 216
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University of Chicago Medical Center 5841 S. Maryland Ave., MC2115, Chicago,
                                                     Contact: Wang SM
                                                                       Chen,J., Lee,S., Zhou,G., Rowley,J.D. and Wang,S.M. A high-throughput GLGI procedure for converting lar SAGE tag sequences into 3' ESTs Unpublished (2001)
                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 197)
                                                                                                                                                                                                                                                   BF942735.1
                                                                                                                                                                                                                                                                             BF942735 197 bp mRNA linear EST-CD15N-040 human CD15+ myeloid progenitor cells Homo sapiens cDNA 3', mRNA sequence.
                                                                                                                                                                                               Homo sapiens
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Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mine
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Keele,J.W.

Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
Unpublished (2000)
                                                                                                                                                                                                                  numan.
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Fax: 402 762 4390
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Plate: 34 row: F column: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DA, ARS, US Meat Animal Research Center
Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta." 64 c 45 g 77 t
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/clone_lib="MARC 2PIG"
/tissue_type="pooled"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                 GI:15624134
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Pred. No. 1.6e-
0; Mismatches
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Best Local Sim
Matches 126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 TTTTTTCCTATGGAAGCATGTTTATAGTGTTCATCAAAGTGCCATAACAGCAACTGAAA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 TAAGGAATTGTTTTGGAAGAGGTGGCTGTTGCAAATCGTTTCTTTTTATAGTGTTCT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 TTTTTCCCTATATTACTATGTTCTGTTCCATTCAAAAAACCGCCTTGCAGACCACAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAATACCATG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGATGCCATCTGCTGGATTCCTGTATTTGTAGTTAAAATCCTTTCCCCTCTTCCGGGTGG 187
                                                                     Contact: Repair Termail.nih.gov
Email: cgapbs remail.nih.gov
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                     IMAGE Consortium (info@image.llnl.gov)
Insert Length: 651 Std Error: 0.00
Seq primer: -40Up from Gibco
High quality sequence stop: 276.
                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
1 (bases 1 to 286)
                                                                                                                                                                                                                                                                                                                                                                                                                                        3', mRNA sequence.
AI375172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 773-702-3002

Email: swangl@midway.uchicago.edu

Email: swangl@midway.uchicago.edu

This EST fragment was amplified from human CD15+ myeloid progenitor

cells cDNA Library with GLGI technique (Generation of Longer cDNA

fragments from SACE tags for Gene Identification, Proc. Natl. Acad.

Sci. USA 97, 2000), which starts from the 3' end till the last

CATG site of the target cDNA sequence.

Seq primer: M13 Forward.
                                                                                                                                                            Contact: Robert Strausberg,
                                                                                                                                                                                  Unpublished (1997)
                                                                                                                                                                                                          Tumor Gene Index
                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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26; Conservative
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quality sequence stop:
Location/Qualifiers
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Non-directionally cloned into UDG sites. Size-selected on agarose gel, average insert size 500 bp. Primary library.
cDNA Library Preparation: David B. Krizman, Ph.D.
REFERENCE: Krizman et al. (1996) Cancer Research
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note="Organ: thyroid; Vector: pAMP10; mRNA
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db_xref="taxon:9606"
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Pred. No. 8.5e-12;
0; Mismatches 64;
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RESULT 6
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 456)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               uy58h08.yl McCarrey Eddy IMAGE:3663807 5' similar
                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF021857.1 GI:10753189
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314 286 1810
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/tissue_type="Pooled human melanocyte, fetal heart,
pregnant uterus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE: 2063423"
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/db_xref="taxon:9606"
/strain="CD-1"
/db_xref="taxon:10090"
/clone="IMAGE:3663807"
                                                                                                                                                                                     Location/Qualifiers
                                                                                                           organism="Mus musculus"
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98.6%;
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3.3e-07;
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BB632910 RIKEN full-length enriched, adult male hypothalamus
musculus cDNA clone A230094D06 5', mRNA sequence.
BB632910
                                                                                                                                                         Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N.,
                                                                                                                            Fax: 81-45-503-9216
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/dev_stage="60_day"
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/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lab_host="DH10B (phage-resistant)"
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Pred. No. 0.
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        Sugahara,Y.,
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                                                                                                                                                                                                                                       AGGTACCATAACCTCTTGGGTAGTGATTGGTTATTCTGCCATTAACAGTGCTTTGAACCC 308
                                                                                                                                   CATCCTCTACACTCTGACGACCTCCTTTTTTAAGGACAAGTTGAAACAGTTGCTGCACAA 185
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450 bp mRNA linear EST 29-JUN-1995
ym37b10.r1 Soares infant brain 1NIB Homo sapiens cDNA clone
IMAGE:50195 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Genome Sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y. and Hayashizaki, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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                                                                                                                                                                                                                                                                                                                                                                                  hypothalamus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="adult
/lab_host="DH10B"
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/dev stage="adult"
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/clone_lib="RIKEN full-length enriched, adult male
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Pred. No. 0.032;
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345 GATAAACCCTGA 356
                                   248 CAGGTACCATAA 259
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                                                                   TTGGGAAAAGAATTCCTAATGTGCTACTAGAATTCCTTCTTCAGTTTTAACGAGTAATTG 344
                                                                                                       CATTATGCTGGATACCCATTTTTGTAGCGAAACCTCTTTCACTGCTTCAGGTAGAAATAC
                                                                                                                                                                               ATCAAGTTAAAAAAGAGATGATCCTTGCCAAACGTTTTTTCTTTATAGTATTTACTGATG
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                                                                                                                                                                                                                                                                                                TTTGTTTTGGGGTGTTTCCAATTTGGATTTTTTTTCCCTGCATCTATCCTCTAAGTTGTTT 164
                                                                                                                                                                                                                                                                                                                                    TTTATTCAGTGGCAATTTTTCTTGGTATTAATTTGGCCGCATTTATCATCATAGTTTTTT 67
                                                                                                                                             GGCCAATCTAAAGGGAAAAATCCTACACTACTTTTACTACTTTTGATTATTTCTCATTT
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H17265.1
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 396.
Location/Qualifiers
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Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hillier, L., Clark, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stops:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
Insert Size: 1886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
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Mammalia; Eutheria;
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/sex="female"
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/db_xref="GDB:423005"
/db_xref="taxon:9606"
/clone="IMAGE:50195"
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Primates;
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                                                                                                                          CATCTGGGGGGAAATGT 444
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                                                                                                                                                                                                          ACTACAGACAAAGAAATCTATGGACAGCAAAGGTATCAGAAAACATATGCTCCATCATT 427
                                                                                  CTGCTGAGGAGATATTT 179
                                                                                                                                                                                                                                                  CATTIAGCGATATCACCACTAACAATTCTGTTAACCATTTTCTTAACCAATGTTGTCATA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
plate: 1101 row: P column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                401 Queen Anne Avenue North, Seattle, Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Mahairas GG, Wallace JC, High Throughput Sequencing Center University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 572)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. au
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HS_5525_B2_H10_T7A_RPCI-11 Human Male_BAC_Library Homo sapiens
genomic_clone_Plate=1101_Col=20_Row=P, DNA_sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            scanning the human genome Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: T7
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Male blood DNA was isolated from one randomly chose
and partially digested with a combination of EcoRI
EcoRI Methylase. Size selected DNA was cloned into
pBACe3.6 vector at EcoRI sites"

a 111 c 84 g 178 t 11 others
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/clone_lib="RPCI-11 Human Male B
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|db_xref="taxon:9606"
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                                                                                                                                                                                                                                                            733 SAAAASAAAYYAAAACTCSYWMCHHTTTTHTTTTATAMTCSAAAGWAKTTATWTTTTATB 674
                                                                                                                                                                                                                                                                                                                                    793 WAWWVWAGTYHTTWCSASYSATATTTTKAACVBGAMTHAATACMCMGASSCWYTTAASYY 734
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                                                                                                                                     ATAACTACAGACAAAGAAAA 384
                                                                                                                                                                                                                    ACCCAATTCTCTATACTCTGACCACAAGACCATTTAAAGAAATGATTCATCGGTTTTTGGC 364
                                                                                                                                                                                                                                                                                               TACCAGGTACCATAACCTCTTGGGTAGTGATTGGTTATTCTGCCATTAACAGTGCTTTGA
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                                                                                                 ATKRAGAAAANAAANRNGA
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bueoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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AL107199
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Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre
BP 191 91006 EVRY cedex - FRANCE (E-mail:
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Drosophila melanogaster genome sur
BACN16A06 of DrosBAC library from
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/plasmId="pBeloBAC11"
/note="end : SP6"
a 178 c 59 g
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/db_xref="taxon:7227"
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Pred. No. 2;
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survey sequence SP6 end of BAC
rom Drosophila melanogaster (fruit
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segref@genoscope.cns.f:
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                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seqref@genoscope.cns.fr - Web :
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exignus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Varrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.

location/Qualifiers
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Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
1 (bases 1 to 896)
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AL440253.1 GI:12223664
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Candida tropicalis, genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (08-SEP-2000)
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Blandin,G., Ozier-Kalogeropoulos,O., Wincker,P., Artiguenave,F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 rue Gaston Cremieux,
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    Conservative
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                                                                                                                                                                                /note="similar to Saccharomyces cerevisiae
SSA4 ; heat shock protein of HSP70 family,
/evidence=not_experimental
                                                                                                                                                                                                                                                                            /note="similar to Saccharomyces cerevisiae ORF YAL005c SSA1; heat shock protein of HSP70 family, cytosolic] similar to Saccharomyces cerevisiae ORF YLL024c [ SSA2 heat shock protein of HSP70 family, cytosolic]"
                                                                                                                                /note="similar to Saccharomyces cerevisiae
SSA3; heat shock protein of HSP70 family,
                                                                                                                                                                                                                                                                                                                                                                                              /organism="Candida tropicalis"
/strain="CBS 94"
/db_xref="taxon:5482"
/clone="BDOAA011A11"
/clone_lib="BDOAA"
                                                                                          /evidence=not_experimental
165 c 139 g 250 m
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                    43.2%;
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                    Score 42.2; DB 17;
Pred. No. 2.3;
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    Mismatches 111;
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                                    Length 896;
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/note="end : T7"
123 c 4 g
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/clone="BACN11016"
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                                                                                                                                                                                                                                                                                                         Local Similarity
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 <u> ҮАНҮҮМИҮҮМИАҮҮМИҮСТАСТҮНҮННННҮНШАҮНТТЖҮАМАНАМИМИННАНҮАААААЖ</u>
                                  TGCTTCAGGTAGAAATACCAGGTACCATAACCTCTTGGGTAGTGATTGGTTATTCTGCCA 289
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                                                                                         TTATAGTATTTACTGATGCATTATGCTGGATACCCCATTTTTGTAGCGAAACCTCTTTCAC 229
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                                                                      AHAAAWWTTHTWWTHAYHWATYHYYYYMYCAMMCMCTHTCHHCYYYYYHHYTAHHTHTHHW 718
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Neopteara; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

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/note="end : TET3"
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/db_xref="taxon:7227"
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839 WYHHTWMHTTTHWAWHTHTWCWWWHATTWTWATHCWACMTMHWHHMHMHHHHMACH
244 CATTTCTCAAAAGAAATATATGCACAGCAAAGATATACGAAAAGATGCTCAACATCATT
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76; Conserv
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High quality sequence stop: 553
Location/Qualifiers
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Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2151 row: D column: 8
Seq primer: T7
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High Throughput Sequencing Center
University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 553)
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HS_2151_B2_B04_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2151 Col=8 Row=D, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Dases 1 to 555)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Keller.A. Shaker,R., Furlong,J., Young,J., Zhao,S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      granning the human genome
Proc. Natl. Acad. Sci. U.S
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                                                                                                                                                                                                                                                                                                      /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones B-Coli DH10B" 90 c 89 g 136 t 8 others
                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/clone="Plate≈2151 Col=8 Row=D"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
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Pred. No. 8.4;
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Search completed: February 3, 2003, 14:18:56
Job time : 1947 secs
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                                                                                                                                                                                                                                                                                                                                                                  ery Match 8.4%; Score 39.8; DB 12; Length 195; St Local Similarity 52.0%; Pred. No. 9.8; atches 89; Conservative 0; Mismatches 82; Indels 0
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                                                                                                                       143 AGATGATCCTTGCCAAACGTTTTTTTTTTATAGTATTTACTGATGCATTAT 193
                                                                                                                                                                                    127 GCCTAAAGGATTATTTTATTGAAATGÁCTGGÁÁAGGÁÁATAGGTTCTCÁÁGAAÁÁAAAÁT 68
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                                                                                            AGAAAATCCATTTTTCACAACTATTTTGTATACATTATTGACTTGCATTTT 17
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 195)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9316 row: d column: 19
High quality sequence stop: 193.
Location/Qualifiers
1 105
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BP178875
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/clone="IMAGE:4038114"
/clone_lib="NCI CGAP Mam5"
/tissue_type="tumor, gross tissue"
/dev stage="7 months"
/lab_host="DH10B"
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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                           GenCore version 5.1.3 (c) 1993 - 2003 Compugen Ltd.
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US-08-853-659A-6
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US-08-91-789A-29
US-09-134-001C-123
US-09-134-001C-123
US-09-134-001C-123
US-09-134-001C-123
US-09-131-79
US-08-91-711-3
US-09-791-211-3
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AAAGTGCCATAACAGCAACTGAAATACGGAATCAAGTTAAAAAAGAGATGATCCTTGCCA 157

Query Match 8.1%; S Best Local Similarity 62.5%; P Matches 60; Conservative 0;	RESULT 1 US-08-853-659A-28/c US-08-853-659A-28/c ISequence 28, Application US/08853659A Patent No. 5925522 GENERAL INFORMATION: A Salmonella Sequence, ITILE OF INVENTION: Of A TITLE OF INVENTION: A Salmonella Sequence, ITILE OF INVENTION: Salmonella Sequence, ITILE OF INVENTION: Salmonella Sequence, ANDRESSE: FOR INTELLE OF INVENTION: Salmonella Sequence, ANDRESSE: Intellectual Property Services ADDRESSE: Hattelle Memorial Institute ADDRESSE: Battelle Memorial Institute STATE: Washington Way CITY: Richland STATE: Washington Way CITY: Richland STATE: Washington Way CITY: Richland COUNTRY: U.S.A. ZIP: 99352 COMPUTER READABLE FORM: COMPUTER READABLE FORM: COMPUTER: BIM PC/XT/AT OPERATING SYSTEM: MS-DOS SOCTWARE: Word Processor (WordPerfect 5.1 CURRENT APPLICATION NUMBER: US/08/853,659A FILING DATE: Unknown CLASSIFICATION NUMBER: DON APPLICATION NUMBER: DON APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION POR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS: LENGTH: 1797 bases TYPE: muclectide STRANDEDNESS: double stranded TOPOLOGY: linear FEATURE: OTHER INFORMATION: the coding nuclectides OTHER INFORMATION: NO:28 correspond to nucleotides OTHER INFORMATION: 24426 of SEQ ID NO:2	28 32.2 6.8 8700 2 29 32.2 6.8 8700 2 31 31.8 6.7 665 2 32 31.8 6.7 1300 4 32 31.6 6.7 48974 4 35 31.4 6.6 290 4 35 31.2 6.6 5009 4 37 31.2 6.6 9717 4 38 31.2 6.6 9717 4 38 31.2 6.6 500 2 C 41 31 6.5 500 2 C 41 31 6.5 500 2 C 42 31 6.5 500 4 C 42 31 6.5 500 4 C 43 31 6.5 500 4 C 44 31 6.5 500 4 C 45 31 6.5 500 4 C 45 31 6.5 500 4
ocore 38.4; DB 2; Length 1797; red. No. 0.25; Mismatches 36; Indels 0; G	US/08853659A i Saffer, J.D. A Salmonella Sequence, Methods Of Detection of A Salmonella Sequence, And Methods Of Detection for Simmerman Stual Property Services Memorial Institute D. Box 999 Way Way Way US/08/853,659A US/08/853,659A Inone Ho: 28: CS: CS: CS: CS: CS: CS: CS: CS: CS: CS	US-08-392-625-16 US-08-466-961A-16 US-08-466-961A-16 Sequence US-08-645-193B-18 Sequence US-08-936-165A-253 Sequence US-08-936-165A-253 Sequence US-08-936-165A-253 Sequence US-08-9106-568E-5 US-09-106-568E-5 US-09-1251-645-1 US-08-967-101-93 US-08-967-101-93 US-08-967-101-93 US-08-967-101-93 US-08-127-480-93 US-09-127-480-93 US-09-124-698-93 US-09-124-698-93 US-09-124-698-93 US-09-124-593 US-08-9124-593 US-08-9124-593 US-08-9124-593 US-08-117-083-23 US-08-117-083-23 US-08-117-083-23 Sequence US-08-117-083-23
Gaps 0;	on Of Salmonella	16, Appl 16, Appl 16, Appl 36, Appl 253, Appl 2, Appl 13, Appl 13, Appl 11, Appl 11, Appl 10, App 93, Appl

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US-08-853-659A-6/c
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              GENERAL INFORMATION:
APPLICANT: Wong, K.F.
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                  Sequence 9, Application US/08853659A
Patent No. 5925522
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection TITLE OF INVENTION: Of A TITLE OF INVENTION: Of A TITLE OF INVENTION: Salmonella Sequence, Methods Of Detection NUMBER OF NOTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: Unknown CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
COMPUTER: IBM PC/XT/AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Word Processor (WordPerfect 5.1) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                   7124 AAATTGCCATAAAAAGAGATGAAAAAAAAGTATTAGTATAAAAAATCTTGTTCATCGATA 7065
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                                                                                                                                                                                                                7064 AAGAGTTTTTTATGATATTTTTTTACTCTTATACTAT
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NUMBER OF SEQUENCES:
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CITY: F
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleotide STRANDEDNESS: do
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: MS-DOS
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                                                    K.K.; Saffer, J.D.
N: A Salmonella Sequence, Methods Of Detection
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 Of A
Salmonella Sequence,
67
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Pred. No. 0.37;
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                    And Methods Of Detection Of Salmonella
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                                                                                                        COUNTRY: U.S....
ZIP: 99352
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.50", 1
MEDIUM TYPE: IBM PC/XT/AT
MS-DOS
WOOT
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 8967 bases
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PRIOR APPLICATION DATA:
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OPERATING SYSTEM: WS-DOS
SOFTWARE: Word Processor (WordPerfect
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette 3.50", 1.44 Mb
COMPUTER: IBM PC/XT/AT
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                         COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PROCESSOR (WordPerfect 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/853,659A
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Intellectual Property Services
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Patent No. 5925522
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Best Local Similarity
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Best Local :
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                                                                                                                                                                                                                                        FILING DATE: n/a
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 8967 bases
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/853,659A
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TITLE OF INVENTION: A Salmonella Sequence,
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Salmonella Sequence, An
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                                                1844 AAAUUGCCAUAAAAAGAGAUGAAAAAAAGUAUUUAGUAUAAAAAAUCUUGUUCAUCGAUA 1903
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ADDRESSEE:
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Intellectual Property Services
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                                                                                                             Score 38.4; DB 2;
Pred. No. 0.37;
3; Mismatches 36;
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Pred. No. 0.37;
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                                                                                                                                                                                                                                                                    RESULT 7
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                                                                                                                                                                          Sequence 3, Application US/08853659A Patent No. 5925522
GEMERAL INFORMATION:
APPLICANT: Wong, K.K.; Saffer, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                           22858 AAATTGCCATAAAAAGÄGATGAAAAAAAGTATTTAGTATAAAAAATCTTGTTCATCGATA 22799
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                        22798
              CORRESPONDENCE ADDRESS:
ADDRESSEE: Paul W. Zimmerman
ADDRESSEE: Intellectual Property Services
ADDRESSEE: Battelle Memorial Institute
ADDRESSEE: PNNL P.O. Box 999
                                                                                                  APPLICANT: Wong, K.K.; Saffer, J.D.
TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection
NUMBER OF SEQUENCES: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 1
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                       158 AACGTTTTTTCTTTATAGTATTTACTGATGCATTAT 193
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RY: Washington
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Word Processor
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N: A Salmonella Sequence, Methods Of Detection
                                                                                                       Of A
Salmonella Sequence, And Methods Of Detection Of Salmonella
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Marches 60; Conserva
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                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
FILING DATE: n/a
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 24701 bases
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                               COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Processor (WordPerfect 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/853,659A
FILING DATE: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE: Paul W. Zimmerman
ADDRESSEE: Intellectual Property Services
ADDRESSEE: Battelle Memorial Institute
ADDRESSEE: PNNL P.O. Box 999
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LENGTH: 24701 bases
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: Unknown
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MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
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   STRANDEDNESS:
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single stranded
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N: A Salmonella Sequence, Methods Of Detection

N: Of A

N: Salmonella Sequence, And Methods Of Detection
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62.5%;
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Pred. No. 0.
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GENERAL INFORMATION:
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Best Local (
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 24701 bases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wong, K.K.; Saffer, J.D.
TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection
NUMBER OF SEQUENCES: 67
                                                                       1844 ÄÄÄUUGCCAUÄÄAÄAGÄGAUGÄÄÄAÄAAGÜAUUUÄGUAUÄÄÄÄÄAAUCUUGUUCAUCGAUÄ 1903
1904 AAGAGUUUUUUAUGAUAUUUUUUUACUCUUAUACUAU 1939
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APPLICATION NUMBER: none
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                                 158 AACGTTTTTTCTTTATAGTATTTACTGATGCATTAT 193
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                                                                                            98 AAAGTGCCATAACAGCAACTGAAATACGGAATCAAGTTAAAAAAGAGATGATCCTTGCCA 157
                                                                                                                                           Local Similarity nes 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Processor
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ZIP: 99352
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Intellectual Property Services
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                                                                                                                                                                                                                                                     single stranded
                                                                                                                                                              38.5%;
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                                                                                                                                                              Score 38.4; DB
Pred. No. 0.48;
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Pred. No. 0.48;
                                                                                                                                             Mismatches
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RESULT 10 US-08-991-789A-169/c ; Sequence 169, Application US/08991789A ; Patent No. 6225054

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                                                                                                                                                                                                                                                                             RESULT 11
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                                                                                                                                                          Sequence 169, Application US/09062451
Patent No. 6344550
GENERAL INFORMATION:
APPLICANT: Frudakks, Tony N.
APPLICANT: Smith, John M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (206) 682-6
INFORMATION FOR SEQ ID NO: 169
SEQUENCE CHARACTERISTICS:
                                                                                         TITLE OF INVENTION: COMPOSITION TITLE OF INVENTION: TREATMENT NUMBER OF SEQUENCES: 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                  672
                                                                                                                                                                                                                                                                                                                                                                                                         732
                                                                                                                                                                                                                                                                                                                                                                                                                                300 TITGAĄCÇCAĄTICICTĄTĄCTCIGACCACAĄGĄCCATTIĄAĄGĄAĄTGATICĄTCGGTT 359
                                                                                                                                                                                                                                                                                                                                                             360 TTGGCATAACTACAGACAAAGAAATCTATGGACAGCAAAGGTATCAGAAAAACATAT 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 AGAAATACCAGGTACCATAACCTCTTGGGTAGTGATTGGTTATTCTGCCATTAACAGTGC 299
                                        STREET:
                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 169:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/991,789A
FILING DATE: 11-Dec-1997
CLASSIFFICATION: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER NUMBER OF SEQUENCES: 292
                                                                                                                                                                                                                                                                                                                        ATATCAACCCATTGTCAATGCACTGTTTTTCAAAGCATTTAAATAGAGGGTAAAACCCCTT 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Frudakis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90;
                    Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1265 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 210121.419C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP:
Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Washington
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                                                                Frudakis,
Smith, John M.
Smith, John M.
Smed, Steven G.
Reed, Steven G.
ROBERT SAID METHODS FOR THE
NVENTION: COMPOSITIONS AND METHODS FOR THE
NVENTION: TORRITHENT AND DIAGNOSIS OF BREAST CANCER
                                  6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                     SEED and BERRY LLP
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701 Fifth Avenue, Suite 6300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37.8; DB Pred. No. 0.34; 0; Mismatches
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RESULT 12
US-09-598-326-169/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS:
LENGTH: 1265 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6423496
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
APPLICATION NUMBER: US/09/598,326
FILING DATE: 20-Jun-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: POTTET, Jane E.R.
REGISTRATION NUMBER: 33,332
PEREPERENT JONES NUMBER: 33,332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/062,451 FILING DATE: 04-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                              Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Frudakis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATATCAACCCATTGTCAATGCACTGTTTTTCAAAGCATTTAAATAGAGGGTAAAACCCTT 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITGAACCCAATTCTCTATACTCTGACCACAAGACCATTTAAAGAAATGATTCATCGGTT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAATAAAACAGGCTTCAGATTATCTTGGCTTTCATAATTATATTTTTTCTTTTAAAGAAAA 733
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                                                                                                                                                                                                                                                                                   CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                              STREET: 701 Fifth Avenue,
REFERENCE/DOCKET NUMBER: 210121.419D1
                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09598326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   John M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tony N.
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Pred. No. 0
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                                                                                                                                                   Version #1
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FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
LENGTH: 1557
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Matches 90; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1232, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 169
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: unsure
LOCATION: (16)
OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
 1173
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                                                                                                                                                                             337 TTTAAAGAAATGATTCATCGGCTTTTGGCATAACTACAGACAAAGAAAAATCTATIGGACAGC 396
                                                                                                                                                                                                              8.0%;
Local Similarity 54.7%;
es 75; Conservation
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TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTGAACCCAATTCTCTATACTCTGACCACAAGACCATTTAAAGAAATGATTCATCGGTT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGAAATTAATACAGAAGAAATGATTCACTTTATGCATAAAAAATAATAATAATAT 616
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                                                                                                         AAAGGTATCAGAAAAACATATGCTCCATCATTCATCTGGGGGAAATGTGGCCACTGCAGG 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGGCATAACTACAGACAAAGAAATCTATGGACAGCAAAGGTATCAGAAAACATAT 416
                                                                                                                                                  TTCAACGAGTAATTTACTCTTTTGTGGGATACCACCAGACGCATACACTGTATGAACAGG 1234
 ATATECTCGATGAATCA 1157
                                 AGATGCCACCTGAGTTA 473
                                                                        AATATGATTATCTTCAAATTGTTTCATAATTAATTTTGTTCCAAATGCTGTAGCTTCAAT 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1265 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
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: (206) 68
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Pred. No. 0.34
0; Mismatches
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                                                                                                                                                                                                                                            Score 37.8; DB 4; Length 1557; Pred. No. 0.35;
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RESULT 14

CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES:

TREATMENT AND 297

BREAST CANCER

ADDRESSEE:

6300

SEED and BERRY LLP 00 Columbia Center,

701

Fifth Avenue

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US-08-991-789A-290/c
; Sequence 290, Application US/08991789A
; Patent No. 6225054
; GENERAL INFORMATION:
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US-09-062-451-290/c
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                                                                                                                                                                                                                  Sequence 290, Application US/09062451
Patent No. 6344550
GENERAL INFORMATION:
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MERAL INFORMATION: Frudakis, Tony M.
APPLICANT: Frudakis, Tony M.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Reed, STEVEN G.
APPLICANT: REED, TONYENTION: COMPOSITIONS AND METHODS FOR MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1045 TGGAAATTAATACAGAAGAATGATTCACTTTATGCATAAAAATAATAATAATAATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 TTGGCATAACTACAGACAAAGAAATCTATGGACAGCAAAGGTATCAGAAAACATAT 416
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les 90; Conserv
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APPLICATION NUMBER: US/08/991,789A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: POTTET, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 210121.419C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1646 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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TELEFAX: (206) 68
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682-6031
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0; Mismatches
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Pred. No. 0.
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CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,451
FILING DATE: 04-APR-1997
CLASSIFICATION NUMBER: 10/90/062,451
FILING DATE: 04-APR-1997
CLASSIFICATION NUMBER: 31,392
REFISHENCE DOCKET NUMBER: 31021.419C2
REFISHENCE DOCKET NUMBER: 31021.419C2
TELEPHONE: (206) 622-4900
TELEPAX: (206) 622-4900
TELEPAX: (206) 622-6901
TELEPHONE: (206) 622-6901
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-062-451-290
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Search completed: February 3, 2003, 13:02:57
Job time : 62 secs
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Best Local Similarity 50.8%;
Matches 90; Conservative
                                                                                               1045 TGGAAATTAATACAGAAGAATGATTCACTTTATGCATAAAAAATAATAATAT 989
                                                                                                                                                                                          1105 ATATCAACCCATTGTCAATGCACTGTTTTTCAAAGCATTTAAATAGAGGGTAAAACCCCTT 1046
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                                                                                                                                                                                                                                           300 TTTGAACCCAATTCTCTATACTCTGACCACAAGACCATTTAAAGAAATGATTCATCGGTT 359
                                                                                                                                                                                                                                                                                                                    240 AGAAATACCAGGTACCATAACCTCTTGGGTAGTGATTGGTTATTCTGCCATTAACAGTGC 299
                                                                                                                                         360 TTGGCATAACTACAGACAAAGAAAATCTATGGACAGCAAAGGTATCAGAAAACATAT 416
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 200000000
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                                   l number of hits satisfying chosen parameters:
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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*

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10: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*

11: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*

12: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
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Match Length
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CURRENT FILING DATE: 2001-11-21
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PRIOR PILING DATE: 2000-01-31
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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APPLICATION NUMBER: 60/220,963
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OR FILING DATE: 2000-10-02
OR APPLICATION NUMBER: 60/237,037
OR FILING DATE: 2000-10-02
OR APPLICATION NUMBER: 60/237,040
OR FILING DATE: 2000-10-02
OR APPLICATION NUMBER: 60/239,936
OR FILING DATE: 2000-10-13
OR APPLICATION NUMBER: 60/239,935
OR FILING DATE: 2000-10-13
OR APPLICATION NUMBER: 60/239,937
OR FILING DATE: 2000-10-13
OR APPLICATION NUMBER: 60/241,787
OR FILING DATE: 2000-11-08
OR APPLICATION NUMBER: 60/246,474
OR FILING DATE: 2000-11-08
OR APPLICATION NUMBER: 60/246,532
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OR APPLICATION NUMBER: 60/249,216
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OR APPLICATION NUMBER: 60/249,216
OR APPLICATION NUMBER: 60/249,210
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OR APPLICATION NUMBER: 60/236,327
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OR APPLICATION NUMBER: 60/241,785
OR FILING DATE: 2000-10-20
OR APPLICATION NUMBER: 60/244,617
OR FILING DATE: 2000-11-01 OR APPLICATION NUMBER: 60/224,519
OR FILING DATE: 2000-08-14
OR APPLICATION NUMBER: 60/220,964
OR FILING DATE: 2000-07-26
OR APPLICATION NUMBER: 60/241,809
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APPLICATION NUMBER: 60/229,513
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APPLICATION NUMBER: 60/231,413 APPLICATION NUMBER: 60/236,368 FILING DATE: 2000-09-29 FILING DATE: 2000-09-29
APPLICATION NUMBER: 60/237,039
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PRIOR EPILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/227, 182
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PRIOR APPLICATION NUMBER: 60/24, 218
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US-09-764-853-137
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; SEQ ID NO 137
; LENGTH: 530
; TYPB: DNA
; ORGANISM: Homo sapiens
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TITLE OF INVENTION: Nucleic Acids, Proteil
FILE REFERENCE: PUZO6
CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
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Pred. No. 2.4e-108;
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Anti
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or fil
NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 986
LENGTH: 530
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-877-986
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Best Local Similarity 96.6
Matches 458; Conservative
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                  TGGCATAACTACAGACAAAGAAAATCTATGGACAGCAAAAGGTATCAGAAAACATATGCTC
                                                                                                                                              GAAATACCAGGTACCATAACCTCTTGGGTAGTGATTGGTTATTCTGCCATTAACAGTGCT
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                                                                                 TTGAACCCAATTCTCTATACTCTGACCACAAGACCATTTAAAGAAATGATTCATCGGTTT
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Pred. No. 2.4e-108;
1; Mismatches 13;
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APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN GPCR PROTEINS
FILE REFERENCE: PC-0044 CIP
CURRENT APPLICATION NUMBER: US/09/895,686
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PERL PROGRAM
SOFTWARE: PERL PROGRAM
SEQ ID NO 37
LENGTH: 612
TYPE: DNA
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RESULT 6
US-09-928-175-11
; Sequence 11, Application US/09928175
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NAME/KEY: misc feature
OTHER INFORMATION: Inc
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Pred. No. 9.6e-108;
0; Mismatches 14;
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NAME/KEY: CDS
. LOCATION: (1)..(2046)
; NAME/KEY: sig_peptide
; LOCATION: (1)..(108)
US-09-928-175-11
                APPLICANT: Paszty, Christopher J.
APPLICANT: Gong, Jianhua
APPLICANT: Gong, Jianhua
APPLICANT: Baugherty, Betsy
APPLICANT: Rogers, No. US20020123618A1ma
TITLB OF INVENTION: Leucine-Rich G Protein Con
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 00-129
CURRENT APPLICATION NUMBER: US/09/928,175
CURRENT APPLICATION NUMBER: US/09/928,175
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/224,455
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 42
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US-09-928-175-6
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/224,455
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 2049
                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/09928175
Patent No. US20020123618A1
GENERAL INFORMATION:
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Best Local Similarity 67.4%;
Matches 242; Conservative
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APPLICANT: Passty, Christopher J.
APPLICANT: Gong, Jianhua
APPLICANT: Gong, Jianhua
APPLICANT: Daugherty, Betsy
APPLICANT: Rogers, No. US20020123618Alma
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 00.1229
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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                                                                                                                                                                                                 Coupled Receptor-8 Molecules and
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Sequence 1, Application US/09928175
PATENT NO. US20020123618A1
GENERAL INFORMATION:
APPLICANT: Paszty, Christopher J.
APPLICANT: Gong, Jianhua
APPLICANT: Bugherty, Betey
APPLICANT: Rogers, No. US20020123618A1ma
INTILE OF INVENTION: Leucine-Rich G Protein Cor
ITITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 00-1229
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US-09-928-175-1
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                                                                                   US-09-928-175-1
                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/928,175
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/224,455
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PACENTIN Ver. 2.0
SEQ ID NO 1
LENGTH: 2265
TYPE: NATE:
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Best Local Similarity
Matches 242; Conserv
  Query Match 36.2%;
Best Local Similarity 67.4%;
Matches 242; Conservative
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LENGTH: 2193
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NAME/KEY: CDS
LOCATION: (1)..(2190)
NAME/KEY: 819 peptide
LOCATION: (1)..(108)
                                                                                                  LOCATION: (1)..(2262)
NAME/KEY: sig_peptide
LOCATION: (1)..(108)
                                                                                                                                                            FEATURE:
NAME/KEY: CDS
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Score 171.8; DB 10;
Pred. No. 1.1e-36;
0; Mismatches 117;
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      Indels
                                          Length
                                             2265;
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APPLICANT: Gong, Jianhua
APPLICANT: Gong, Jianhua
APPLICANT: Gong, Jianhua
APPLICANT: Gong, Jianhua
APPLICANT: Daugherty, Betsy
APPLICANT: Daugherty, Betsy
APPLICANT: No. US20020123618Alma
TITLE OF INVENTION: Leucine-Rich G Protein Coupled Receptor-8 Molecules and
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 00-1229
CURRENT APPLICATION NUMBER: US/09/928,175
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/224,455
PRIOR APPLICATION NUMBER: 60/224,455
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 42
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 19
LENGTH: 2214
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(2211)
NAME/KEY: sig_peptide
LOCATION: (1)..(57)
US-09-928-175-19
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Best Local Similarity
Matches 226; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mus musculus
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                              TTATGCTGGATACCCATTTTTGTAGCGAAACCTCTTTCACTGCTTCAGGTAGAAATACCA 249
                                                                                     CACATCGGGAAGGAGGTGGCTGTTGCAAACCGGTTCTTTTTTATCGTGTTCTCTGATGCC 1893
                                                                                                           CAAGTTAAAAAGAGATGATCCTTGCCAAACGTTTTTTCTTTATAGTATTTACTGATGCA 189
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                                                                                                                                                                    TATGTCACCATGTTCTGCTCCATTCATAAAACAGCCCTTCAGACTGCAGAAGTGAGGAGC 1833
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Pred. No. 8e-30;
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APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Baughn, Mariah R.
ITILE OF INVENTION: HUMAN GPCR PROTEINS
FILE REFERENCE: PC-0044 CLP
CURRENT APPLICATION UNMBER: US/09/895,686
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PERL PROGRAM
SEQ ID NO 62
LENGTH: 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
CRCANISM: Rattus norvegicus
FENTURE:
NAME/KEY: misc_feature
COTHER INFORMATION: Incyte ID No. US20020106655A1 702466096T1
US-09-895-686-62
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US-09-895-686-62/c
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APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                             Sequence 169, Application US/09924400 Patent No. US20020165371A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 140; Conserv
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Best Local
                                                                                                                                                                                                                                                                                                                                          GENERAL
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APPLICANT:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                   APPLICANT: Frudakis, Tony N. APPLICANT: Reed, Steven G. APPLICANT: Smith, John M. APPLICANT: Misher, Lynda E. APPLICANT: Dillon, Davin C.
APPLICANT: Deng, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C12
CURRENT APPLICATION NUMBER: US/09/924,400
CURRENT FILING DATE: 2001-08-07
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                                                                                                                                                                                                                                                                                                                                              INFORMATION:
                                                                                                                                                                                                                   Reed, Steven G.
Smith, John M.
Misher, Lynda E.
Dillon, Davin C.
Retter, Marc W.
                                                                                                                                                                             Wang, Aijun
Skeiky, Yasir A.
                                                                                                                     Day, Craig H.
Li, Samuel X.
                                                                                                                                                              Harlocker, Susan
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Pred. No. 1.2e-19;
0; Mismatches 33
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SOFTWARE: FASTSEQ for Windows Version
; SEQ ID NO 169
; LENGTH: 1265
; TYPE: DNA
; ORGANIZM: Homo sapiens
US-09-924-400-169
RESULT 13
US-09-429-755-169/c
; Sequence 169, Application US/09429755A
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CURRENT APPLICATION NUMBER: US/09/810,936
CURRENT FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 334
SOFTWARE: FastSEQ for Windows Version 3.0
TEQ ID NO 169
LENGTH: 1265
TYPE: DNA
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Best Local S
Matches 90
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Patent No. US20020068285A1
GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Reed, Steven G.
APPLICANT: Smith, John M.
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APPLICANT:
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                 672
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                                                                                                                                                                                                                                          300 TTTGAACCCAATTCTCTATACTCTGACCACAAGACCATTTAAAGAAATGATTCATCGGTT 359
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                                                                                                                                                                                                                                                                                       v Match 8.0%; Score 37.8; DB 10; Length 1265;
Local Similarity 50.8%; Pred. No. 0.67;
nes 90; Conservative 0; Mismatches 87; Indels 0;
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les 90; Conserv
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                                                                                                               TGGAAATTAATACAGAAGAATGATTCACTTTATGCATAAAAAATAATAATAATAT 616
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Dillon, Davin C.
Retter, Marc W.
Wang, Aijun
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Harlocker, Susan L.
Day, Craig H.
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50.8%; Pred. No. 0.67;
ative 0; Mismatches 87; Indels 0
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APPLICANT: Misher, Lynda
APPLICANT: Misher, Lynda
APPLICANT: Dillon, Davin C.
APPLICANT: US/09/170N AND METHODS FOR THE
FITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C6
CURRENT APPLICATION NUMBER: US/09/429,755A
CURRENT FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 315
SOFTMARE: FRASEQ for Windows Ver-
SEQ ID NO 169
LENGTH: 1265
TYPE: DNA
OPC.
                                APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Day, Craig H.
APPLICANT: Li, Samuel X.
APPLICANT: Li, Samuel X.
APPLICANT: Derg, Ta AND DIAGNOSIS OF BREAST CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C12
CURRENT APPLICATION NUMBER: US/09/924,400
CURRENT FILING DATE: 2001-08-07
NUMBER OF SEQ ID NOS: 340
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 290
LENGTH: 1646
TYPE: DNA
ORGANISM: Homo sapiens
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US-09-924-400-290/c
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Query Match 8.0%;
Best Local Similarity 50.8%;
Matches 90; Conservative
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APPLICANT:
APPLICANT:
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Local Similarity 50.8%;
les 90; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAATAAAACAGGCTTCAGATTATCTTGGCTTTCATAATTATATTTTTCTTTTAAAGAAAA 733
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Wang, Aijun
Skeiky, Yasir A. W.
Harlocker, Susan L.
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Dillon, Davin C.
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Pred. No. 0.67;
0; Mismatches 87;
  0;
Score 37.8; DB Pred. No. 0.74; O; Mismatches
    87;
                                         Length 1646;
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    Indels
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240 AGAAATACCAGGTACCATAACCTCTTGGGTAGTGATTGGTTATTCTGCCATTAACAGTGC 299

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APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, John M.
APPLICANT: Misher, Linda E.
APPLICANT: Misher, Linda E.
APPLICANT: Misher, Linda E.
APPLICANT: Misher, Linda E.
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Day, Craig H.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Wang, Aljun
APPLICANT: Wang, Alju
Search completed: February 3, 2003, 14:20:03 Job time : 59 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.0%; Score 37.8; DB 10; Length 1646; Best Local Similarity 50.8%; Pred. No. 0.74; Matches 90; Conservative 0; Mismatches 87; Indels 0;
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                                                                                                                                                                                         1045 TGGAAÁTTÁATÁĆÁGÁAGAAATGÁTTCACTTTÁTGCATÁÁAAAAÁTAÁATAÁTAATÁT 989
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution to have a being printed,

10	9	89	7	6	տ	4	w	N	ú	Result No.
632	632	632	638	638	638	638	638	638	826	Score
76.5	76.5	76.5	77.2	77.2	77.2	77.2	77.2	77.2	100.0	% Query Match
								188		% Query Match Length DB
22	22	22	20	20	22	21	22	22	22	B
ABB04062	AAM99972	AAU87545	AAY42170	AAY42171	AAE02498	AAY57286	AAU87243	AAM99945	AAB35407	SUMMARIES
Human musculoskele	Human expressed po	Novel central nerv	Human LGR7 long fo	-	Human CON222 G pro	Human GPCR protein	Novel central nerv	Human expressed po	Human HGRL101 G-pr	Description

Novel G-coupled protein receptor, HGRL101 useful for treating diseases

WPI; 2001-226617/23. N-PSDB; AAF28059.

Duecker K;

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
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AAR30521	AAR30519	AAR30513	AAR30525	AAR30524	AAR30506	AAR08038	AAR30514	AAR30509	AAR30520	AAR30522	AAM47959	AAU38931	ABB61216	AAU38929	ABB60463	AAG80961	AAE20168	AAE20148	AAE20167	ABB06254	AAU97158	ABB06255	AAU97159	ABB06250	ABB06251	ABB06252	ABB06253	AAU04370	AAB41526	AAU21646	AAU18666	AAU18344	AAU18108	ABB10249
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ALIGNMENTS

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RESULT 1

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RESULT 2
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     31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
19-MAY-2000;
07-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences for a novel human G-protein coupled receptor, designated HGRL101. The sequences are useful in the diagnosis, prevention and treatment of diseases including infections, pain, cancer, diabetes, amorexia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypotrension, urinary retention, osteoporosis, angina pectoris, myocardial infearction, stroke, ulcers, allergies, benign prostatic hypertrophy, migraine, vomiting, psychotic and neurological disorders such as anxiety, schizophrenia, manic depression, depression, delirium, dementia and severe mental retardation, and dyskinesias including Huntington's disease and Gilles dela Tourette's syndrome. The present sequence is the HGRL101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            such as micro
hypotension,
allergy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibaccerial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticorvulsant; antifungal; antiparastic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                 17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                       02-AUG-2001
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157; Conserv
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2000US-0199076.
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1. No. 1e-88;
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01-DEC-2000
08-DEC-2000
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                                                                             diagnosis
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DB; AAI99557.
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                                                                                                                                                                                                     SCI INC
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                                                     509pp
                                                                                                                                                                             SM;
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Isolated digestive system associated polypeptide for treating, preventing and/ or prognosing disorders related to the digestive system including digestive system cancers and also for testing and detection

Sequence Listing; English

1-JAN-2000; 04-FEB-2000; 24-FEB-2000; 24-FEB-2000; 16-MAR-2000; 11-MAR-2000; 11-APR-2000; 19-MAY-2000; 28-JUN-2000;

; 2000US-0180628. 2000US-0194664. 2000US-0186350. 2000US-019974. 2000US-019976. 2000US-0199123. 2000US-0205467. 2000US-0209467. 2000US-0214886.

17-JAN-2001;

2001WO-US01332 2000US-0179065

The invention relates to novel genes (AAI99548-AAI99604) and proteins (AAM99936-AAM99984) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification

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Best Local Sim
Matches 127;
                                                                                                                                                                                                                                                                                                                      Central nervous system; CNS; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
                                                                                                                                                                                                                                                                             encocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder myocardial infarction; wound healing; cell proliferation; skin aging food additive; food preservative; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infections diseases such as viral, bacterial, fungal and parasitto infections.
                                                                                                                                                                                                                        WO200155318-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                             central nervous system protein #153.
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27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
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No. 1.4e-66;
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tronic format directly
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                                                                                                                                                                                                                                                                                                           disorder;
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2000US-0215135.
2000US-0216807.
2000US-0217487.
2000US-0217496.
2000US-022964.
2000US-0224519.
2000US-0224519.
2000US-0225214.
2000US-0225214.
2000US-0225266.
2000US-0225267.
2000US-0225267.
2000US-0225275.
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30-JUN-2000; 07-JUL-2000; 07-JUL-2000; 11-JUL-2000; 11-JUL-2000; 14-JUL-2000; 26-JUL-2000; 26-JUL-2000;

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17-NOV-2000)
17-NO
                                                                                                                                                        New isolated nu-
preventing, tre-
food additives
The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
                                                                                                                                                                                                                             WPI; 2001-581633/65.
N-PSDB; ABK43573.
                                                                                                                                                                                                                                                                                  Rosen
                                                                                                                         Claim
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2000US-0246610

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2000US-0246611

2000US-024920

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2000US-02511866
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                                                                                                                           English.
                                                                                                                                                                                protein for diagnosing, medical conditions and
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14-AUG-2000)
130-AUG-2000)
101-SEP-2000)
102-SEP-2000)
103-SEP-2000)
104-SEP-2000)
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2000US-023299 2000US-023513 2000US-0231443 2000US-0231443 2000US-0231443 2000US-0231443 2000US-0231443 2000US-0231461 2000US-023298 2000US-023299 2000US-023299 2000US-023299 2000US-0232400 2000US-0232401 2000US-023361 2000US-023361 2000US-0234201 2000US-0234203 2000US-0236367 2000US-0236367 2000US-0236367 2000US-0236367 2000US-0236369 2000US-023680 2000US-

Claim 1; Page 62-63; 71pp; English

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RESULT 4
AAY57286
ID AAY5
XX AAY5
AC AAY5
XC AAY5
XX Huma
XX Huma
XX Huma
XX Huma
XX Huma
XX Anti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; G protein coupled protein receptor; HGPRP; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human GPCR protein (HGPRP) sequence (clone ID 2488822).
                 Human G protein coupled protein receptor peptides useful for the prevention, diagnosis and treatment of cell proliferative, neuro
                                                                                                                                                                   Bandman O,
Baughn MR;
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                                                                                            N-PSDB; AAZ90524.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                      (INCY-) INCYTE
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immune disorders
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94.8%;
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1; Mismatches
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Pred. No. 1.7e-66;
                                                                                                                                                                                          Corley NC,
                                                                                                                                                                                        Guegler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
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                       neurological
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention provides human G protein coupled protein receptor (HGPRP) polypeptides and polymucleotides encoding them. The polypeptides can be produced by standard recombinant methodology. The polymucleotides and polypeptides may be used in the prevention, treatment and diagnosis of diseases associated with their inappropriate expression. Diseases that can be treated are cell proliferative disorders (e.g. arteriosclerosis, atherosclerosis and hepatitis), cancers (e.g. leukemia, melanomas and adenocarcinoma), immune disorders (e.g. ania, asthma and Crohn's disease) and neurological disorders (e.g. epilepsy, Alzheimer's disease and parkinson's disease). The anti-hGPCR antibodies may also be used as diagnostic agents for detecting the presence of HGPRP polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). Sequences AAY57283-288 represent the HGPRP polypeptides.
                                                                                                                                                                                                                                                                                                                                                Human; G protein-coupled receptor; GPCR; CON222 protein; schizophrenia; neuroleptic; nootropic; neuroprotective; bipolar disease; psychotropic; neurological disorder; psychiatric disease; neurosis; anxiety; neuritis; attention deficit hyperactivity disorder; neurasthenia; senile dementia; affective disorder; neuropathy; Alzheimer's disease; Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE02498 standard; Protein; 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human CON222 G protein-coupled receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-AUG-2001
                             Domain
                                                                                                                                                                                                                                                                                                                                  depression; migraine; genetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 AQIYSVAIFIGINLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity es 127; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AQIYSVAIFLGINLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVF
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                             /note=
                                                                                                                                                                                                                                            /labe
                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                /label= Intracellular_domain
/note= "First IC loop"
                'label=
                                                           /label≃
                                                                                     label= Transmembrane_domain_(3TM)
                                                                                                                      /label= Extracellular_
/note= "First EC loop"
                                                                                                                                                                  'label= Transmembrane_domain_(2TM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348
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                              188
                                                                                                                                                                                                                                         l= Transmembrane_domain_(1TM)
            _Transmembrane_domain_(4TM)
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Pred. No. 3.8e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                       screening.
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                                                                                                                                      _domain
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3.8e-66;
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Best Local S
Matches 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seven transmembrane receptor polypeptides and polynucleotides, useful for treating neurological or psychiatric disorders, e.g. schizophrenia, as well as for identifying compounds useful for treating schizophrenia
                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 15-16; 215pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PHAA ) PHARMACIA &
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                 61
                                           AQIYSVAIFLGINLAAFIIIVESYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVF 60
TDALCWIPIFVAKPLSLLQVEIPGTITSWVVIGYSAINSALNPILYTLTTRPFKEMIHRF 120
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                                                                                                          al Similarity
127; Conser
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99US-0429555.

99US-0429676.

99US-0429695.

99US-0429695.

99US-0454399.

2000US-0481794.
                                                                                                        Conservative
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                                                                                                                                                                    AA;
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/note= "Second EC loop"
217..241
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/note= "Third EC loop"
301..320
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/note= "Third IC loop"
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                                                                                                                     77.2%;
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                                                                                                     Score 638; DB 22;
Pred. No. 3.8e-66;
1; Mismatches 6
                                                                                                                                       DB 22;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents the human G-protein coupled receptor having extracellular leucine rich repeat regions, designated LGR7 short form. The LGR4, LGR5 and LGR7 proteins are used to identify ligands for the receptor. The polypeptides and/or polynucleotides are also useful for homologous or related genes, producing compositions that modulate the expression or function of the receptors, gene therapy, mapping functional regions of the receptors, studying associated physiological pathways, in vivo prophylactic and therapeutic purposes, as immunogens for producing antibodies, and for identifying biologically active agents. The polypeptides contain a G-protein coupled seven transmembrane regions capture and facilitate optimal orientation of its ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New G-protein coupled
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; LGR4; LGR5; LGR7; G-protein coupled receptor; gene therapy; extracellular leucine rich repeat region; mapping; identification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human LGR7 short form protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The proteins are also expressed in diverse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-1998;
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                                                                                                                                        61
                                                                                                                                                                                                                            1 AQIYSVAIFLGINLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVF
WHNYRQRKSMDSKG
                                                                                    TDALCWIPIFVVKFLSLLQVEIPGTITSWVVIFILPINSALNPILYTLTTRPFKEMIHRF
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                                                                                                                 TDALCWIPIFVAKPLSLLQVEIPGTITSWVVIGYSAINSALNPILYTLTTRPFKEMIHRF
                                                                                                                                                                                            AQIYSVAIFLGINLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVF
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                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   722 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptors,
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                                                                                                                                                                                                                                                                                                                               Score 638; DB 20;
Pred. No. 8.3e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Van Der Spek PJ;
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                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                               722;
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661 WYNYRQRKSMDSKG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents the human G-protein coupled receptor having extracellular leucine rich repeat regions, designated LGR7 long form. The LGR4, LGR5 and LGR7 proteins are used to identify ligands for the receptor. The polypeptides and/or polymucleotides are also useful for homologous or related genes, producing compositions that modulate the expression or function of the receptors, gene therapy, mapping functional regions of the receptors, studying associated physiological pathways, in vivo prophylactic and therapeutic purposes, as immungens for producing antibodies, and for identifying biologically active genes. The polypeptides contain a G-protein coupled seven transmembrane region and a leucine rich repeat extracellular domain. These regions capture and facilitate optimal orientation of its ligand. The proteins are also expressed in diverse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-591074/50.
N-PSDB; AAZ25345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-SEP-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09948921-A1
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extracellular leucine ric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Fig 3; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New G-protein coupled receptors, useful for identifying their ligands - % \left\{ 1\right\} =\left\{ 1\right\} =\left\{
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hsueh AJW, Hsu SY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-1998;
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969
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                                                                                                                                                                        TDALCWIPIFVAKPLSLLQVEIPGTITSWVVIGYSAINSALNPILYTLTTRPFKEMIHRF 120
                                                             WHNYRORKSMDSKG 134
WYNYRORKSMDSKG 709
                                                                                                                                                                                                                                                                                                                                                                      AQIYSVAIFLGINLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           757 AA;
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leucine rich repeat region; mapping; identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0079501.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 638; עט
Pred. No. 8.8e-
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            638; DB 20;
No. 8.8e-66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60
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RESULT 8

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Central nervous system; CNS; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; ALDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endoorine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; remal disorder; kidney failure; blood disorder; respiratory disorder; remal disorder; kidney failure; blood disorder; remal disorder; call proliferation; skin aging; fold distinction; wound healing; cell proliferation; skin aging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU87545 standard; Protein; 176 AA
Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel central nervous system protein #455
                                                                                             additive;
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                                                                                             food preservative; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
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14-AUG-2000 18-AUG-2000 18-AUG-2000 22-AUG-2000 22-AUG-2000 23-AUG-2000 30-AUG-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 05-SEP-2000 06-SEP-2000 06-SEP-2000 31-JAN-2000; 04-FEB-2000; 24-FEB-2000; 02-MAR-2000; 02-AUG-2001. WO200155318-A2 17-JAN-2001; 2000US-0184664 2000US-0189374 2000US-0199874 2000US-0199874 2000US-0199123 2000US-0205515 2000US-020515 2000US-0214867 2000US-02148647 2000US-0214889 2000US-0217487 2000US-0217487 2000US-0217487 2000US-0217486 2000US-0217486 2000US-0217486 2000US-0217486 2000US-0217486 2000US-0217486 2000US-0225758 2000US-0225759 2000US-0226279 2000US-0226681 2000US-0226888 2000US-0227182 2000US-0227182 2000US-0229343 2000US-0229343 2000US-0229345 2000US-0229345 2000US-0229343 2000US-0229345 2000US-0229345 2000US-0229345 2000US-0229343 2000US-0229345 2000US-0229345 2000US-0229345 2000US-0229343 2000US-0220964 2000US-0224518 2000US-0224519 2000US-0225213 2000US-0225214 2000US-0225266 2000US-0225267 2000US-0225267 2000US-0225270 2000US-0225277 2000US-0225277 2001WO-US01332. 2000US-0179065

08-SEP-2000; 08-SEP-2000; 08-SEP-2000;

2000US-0231243. 2000US-0231244. 2000US-0231413.

08-SEP-2000;

2000US-0232400 2000US-0232401 2000US-0233063 2000US-0233064 2000US-0233065 2000US-0234223 2000US-0234223 2000US-0234274 2000US-0234274

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                                                                                                                                                                                                            Query Match
Best Local
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17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
01-DEC-2000
05-DEC-2000
05-DEC-2000
05-DEC-2000
06-DEC-2000
08-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic preventing, treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME
                             121
                                                             61
                                                                                          61
                                                                                                                                                             بر
                   WHNYRQRKSMDSKG
                                                                                                                          AQIYSVAIFLGINLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-581633/65.
WYNYRQRKSMDSXG
                                                                                TDALCWIPIFVAKPLSLLQVEIPGTITSWVVIGYSAINSALNPILYTLTTRPFKEMIHRF
                                                              TDALCWIPIFVVKFLSLLQVEIPGTITSWVVIFILPINSALNPILYTLTTRPFKEMIHRF
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                                                                                                                                                                                            126;
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                                                                                                                                                                                                              Similarity
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2000US-0251719
2000US-0251479
2000US-0251856
2000US-0251868
2000US-0251869
2000US-0251989
2000US-0251989
2000US-0251989
2000US-0251987
2000US-0251987
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2000US-0249265
2000US-0249297
2000US-0249299
2000US-0249299
2000US-0250160
2000US-0250160
2000US-02501391
2000US-0251030
                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or preservatives
                             134
                                                                                                                                                                                                          76.5%;
94.0%;
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                                                                                                                                                                                         Score 632; DB 22;
Pred. No. 6.7e-66;
l; Mismatches 7;
                                                                                                                                                                                                                        Length
                                                                                                                                                                                              Indels
                                                                                                                                                                                                                             176;
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2000US-0240960 2000US-0241221 2000US-0241785 2000US-0241786 2000US-0241787 2000US-0241809 2000US-0241809 2000US-0241809 2000US-0241809 2000US-0241809 2000US-0241809 2000US-0241809 2000US-0241809 2000US-0241807 2000US-0241807 2000US-0241807 2000US-0241807 2000US-0241807 2000US-0241807

14-SEP-2000
14-SEP-2000
14-SEP-2000
14-SEP-2000
21-SEP-2000
25-SEP-2000
25-SEP-2000
27-SEP-2000
27-SEP-2000
29-SEP-2000
20-OCT-2000
02-OCT-2000

2000US-0246523 2000US-0246523 2000US-0246526 2000US-0246526 2000US-0246527 2000US-0246527 2000US-0246528 2000US-0246632 2000US-0246610 2000US-0246611 2000US-0246611 2000US-0246611 2000US-0246611 2000US-024920 2000US-0249211 2000US-0249211

08-NOV-2000

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RESULT 9
AAM9997
ID AAM99
XX AAM9
XX AAM9
XX Huma
DT 04-J
DX Huma
XX H
       11-JUL-2000;
11-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
15-AUG-2000;
16-AUG-2000;
17-AUG-2000;
18-BP-2000;
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                (AAM99936-AAM99984) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, altoimmune haroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as wyotal, bacterial, fungal and parasitic infections.
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N-PSDB; AAI99584.
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           ABB04062
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                                                                          WYNYRQRKSMDSXG
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Human musculoskeletal system related polypeptide SEQ
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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antialifammatory; antiucer; vulnerary; anticonvulsant; antidiacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; system.

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RESULT 11
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format direfrom WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                              TDALCWIPIFVAKPLSLLQVBIPGTITSWVVIGYSAINSALNPILYTLTTRPFKEMIHRF
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)B; AAL35644.
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7 2000US-0254097

7 2001US-0254097
                                                                                                                                                            Conservative
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                                                                                                                                                                                                                         AA;
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134
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                                                                                                                                                          Score 632; DB 22; Pred. No. 6.7e-66; 1; Mismatches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence Listing; English.
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                                                                                                                                                          7;
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Human; gene the muscular disoparticle of the muscular dispersion disoparticle of the muscular dispersion dispersi
bbc ID NO: 557. therapy, neural disorder; jmmune system disorder; order; reproductive disorder; gastrointestinal disorder; socder; reproductive disorder; renal disorder; socder; ardiovascular disorder; renal disorder; socder; soc
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14-SEP-2000 21-SEP-2000 21-SEP-2000 25-SEP-2000 26-SEP-2000 27-SEP-2000 27-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 20-OCT-2000 20-OCT-2000 20-OCT-2000 20-OCT-2000 20-OCT-2000 20-OCT-2000 20-OCT-2000 20-OCT-2000 20-OCT-2000 21-NOV-2000 20-OCT-2000 21-NOV-2000 21-NOV
2000US-233064P. 2000US-233064P. 2000US-234997P. 2000US-234997P. 2000US-234997P. 2000US-234997P. 2000US-234997P. 2000US-235334P. 2000US-235366P. 2000US-23666P. 2000US-23666P. 2000US-23666P. 2000US-23666P. 2000US-23666P. 2000US-23666P. 2000US-23667P. 2000US-23666P. 2000US-23666P. 2000US-23666P. 2000US-24677P. 2000US-24921P. 2000US-24662P. 2000US-24662P. 2000US-24662P. 2000US-2492P. 2000US-24662P

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RESULT 12
AAU18108
ID AAU16
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Matches 126
31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides human cDNAs, proteins and related genomic DNAs. These can be used in the treatment of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders and inflammation. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-DEC-2000; 2000US-251869P.
08-DEC-2000; 2000US-251989P.
08-DEC-2000; 2000US-25199P.
11-DEC-2000; 2000US-254097P.
05-UAN-2001; 2001US-259678P.
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                                                                                                                                                                           WO200155201-A1
                                                                                                                                                02-AUG-2001
                                                                                                                                                                                                                                           Human; uterine
                                                                                                                                                                                                                                                                    Novel human uterine motility-association polypeptide
                                                                                                                                                                                                                                                                                                 21-NOV-2001
                                                                                                                       17-JAN-2001;
                                                                                                                                                                                                                              labour;
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Local Similarity 94.0%;
les 126; Conservative
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DB; ABA06471.
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2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-018350.
2000US-018974.
2000US-019973.
2000US-0199123.
2000US-0205515.
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                                                                                                                                                                                                                                                                                               entry)
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Pred. No. 6.7e-66;
1; Mismatches 7;
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    07-JUN-2000

28-JUN-2000

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30-JUN-2000

07-JUL-2000

11-JUL-2000

11-JUL-2000

11-JUL-2000

14-AUG-2000

14-SEP-2000

15-SEP-2000

16-SEP-2000

17-SEP-2000

17-SEP-2000

11-SEP-2000

11-SE
 2000US-0229447

2000US-0214886

2000US-0215135

2000US-0215880

2000US-0217487

2000US-0217487

2000US-0217496

2000US-0224519

2000US-0224519

2000US-0224519

2000US-0225267

2000US-0225267

2000US-0225277

2000US-0225757

2000US-0225778

2000US-0225787

2000US-0231413

2000US-0231498

2000US-0231498

2000US-0231498

2000US-0231680

2000US-0231680

2000US-02317039

2000US-02337039

2000US-02337039

2000US-02337039

2000US-0233935

2000US-0233937

2000US-0233937
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20-OCT 2000
20-NOV 2000
20-NOV
The present invention relates to the isolation of novel human uterine motility-association polypeptides, and cDNA (AAS28936 and genomic sequences encoding for these polypeptides. The sequences of the invention are useful in the diagnosis,
                                                                                                                                        Isolated polypeptide and nucleic acid molecules for treating, preventing and/or prognosing disorders related to uterine motility e.g. disorders associated with pregnancy and the menstrual cycle -
                                                                                                        Claim
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                                                                                                        11;
                                                                                                                                                                                                                                                                                            CA,
                                                                                                                                                                                                                                                                                                                                     HUMAN GENOME
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                                                                                                      SEQ ID
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2000US-0249244.

2000US-0249245.

2000US-0249264.

2000US-0249265.

2000US-0249297.

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2000US-0249299.
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2000US-0244809
2000US-0246474
2000US-0246475
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2000US-0246476
2000US-0246477
2000US-0246477
2000US-0246523
2000US-0246523
2000US-0246526
2000US-0246526
2000US-0246527
2000US-0246532
2000US-0246532
2000US-0246610
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2000US-0246611
2000US-0246611
2000US-0249200
2000US-0249211
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2000US-0241786.
2000US-0241787.
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2000US-0254097
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                                                                                                      No 84;
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                                                                                                    524pp; English.
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RESULT 13
AAU18344
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Best Local Similarity
Matches 126; Conserv
Endocrine protein; human; mouse; rabbit; goat; horse; food additive; cat; dog; chicken; sheep; immunosuppressive; antiarthricic; vasotropic; antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective; cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer; ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; breast; liver; cardiovascular disorder; nervous system disorder; bacterial infection; fungal infection; viral infection; ocular disorder; endocrine disorder; gastrointestinal disorder; renal disorder; respiratory disorder; wound healing; skin aging; organ transplantation; food preservative; tissue regeneration; anti-infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treatment, prevention and/or prognosis of diseases associated with uterine motility such as pregnancy and labour, and menstrual disorders. The polynucleotide sequences of the invention are also useful in gene therapy. AAU18094-AAU18152 represent novel human uterine motility-association polypeptides.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                       Human endocrine polypeptide SEQ ID No 299.
                                                                                                                                                                                                                                                                                                                                         21-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU18344 standard;
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                                                                                                                                                                                                                                                                                                                                      (first entry)
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Pred. No. 6.7e-66;
1; Mismatches 7,
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)S Homo sapiens. CX ... WO200155364-A2.

02-AUG-2001. 17-JAN-2001; 2001WO-US01308

31-JAN-2000; 2000US-0179065.
04-FEB-2000; 2000US-0186628.
24-FEB-2000; 2000US-0186350.
16-MAR-2000; 2000US-0186350.
17-MAR-2000; 2000US-0199174.
17-MAR-2000; 2000US-0199123.
19-MAY-2000; 2000US-0199123.
19-MAY-2000; 2000US-0209467.
28-UUN-2000; 2000US-0214886.
30-UUN-2000; 2000US-0214886.
30-UUN-2000; 2000US-0214886.
30-UUN-2000; 2000US-0214890.
11-UUL-2000; 2000US-0214890.
11-UUL-2000; 2000US-0214890.
11-UUL-2000; 2000US-0214890.

2000US-0218290 2000US-0220963 2000US-0220964 2000US-0224518 2000US-0225213 2000US-0225214 2000US-0225214 2000US-0225266 2000US-0225266 2000US-0225267 2000US-0225267 2000US-0225275 2000US-0225447 2000US-0225757 2000US-0225758 2000US-0225758 2000US-0225758 2000US-0225758 2000US-0225758 2000US-0225758 2000US-0225758 2000US-0225758

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Sequences AAU18282-AAU18507 represent endocrine polypeptides of the invention. Endocrine polypeptides and their associated polynucleotides are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by determining the presence or absence of a mutation in an endocrine polynucleotide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, hyperproliferative disorders such as neoplasms of the breast or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as cardiac arrest, and a cardiac arrest of the breast of the presence of a mutation in an endocrine as rheumatoid arthritis, hyperproliferative disorders such as cardiac arrest, cerebrovascular disorders such as cardiac arrest, and the presence of the breast of the presence of the
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17-NOV-2000
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          disorders
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DB; AAS29573.
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2000US-0246527.
2000US-0246532.
2000US-0246609.
2000US-0246611.
2000US-0246611.
2000US-0249209.
2000US-0249209.
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2000US-0249269.
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2000US-0251988.
2000US-0251868.
2000US-0251868.
2000US-0251989.
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2000US-0246476.
2000US-0246477.
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  infections
  caused
nervous system sed by bacteria,
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14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 22-AUG-2000; 22-AUG-2000; 22-AUG-2000; 23-AUG-2000; 01-SEP-2000; 01-SEP-2000;

2000US-0227182. 2000US-0227009. 2000US-0228924. 2000US-0229287. 2000US-0229343. 2000US-0229344.

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14-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 21-SEP-2000 25-SEP-2000 26-SEP-2000 27-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 21-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 20-OCT-2000 20-OC

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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                        Human; antiinflammatory; neuroprotective; immunomodulator; vulnerary; cardiovascular; cytostatic; nephrotropic; antianaemic; nephritis; immunosuppressive; kidney disorder; renal failure; hypertension; cardiovascular disorder; myocardial infarction; blood disorder; anaemia blood coagulation disorder; electrolyte imbalance disorder; cancer; hyponatraemia; hyperkalaemia; neoplastic disorder; nephtoma; autoimmune disease; inflammatory disease; reproductive system disorder; neural activity; neurological disorder; wound healing; respiratory disorder.
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      The invention relates to novel nucleic acids and polypeptides useful fidingnosing, treating, preventing and/or prognosing disorders related these polypeptides. The polynucleotides are especially useful in the diagnosis, prognosis, prevention and/or treatment of diseases which include kidney disorders (e.g. renal failure or nephritis), cardiovascular disorders (e.g. hypertension or myocardial infarction), blood disorders (e.g. annemia or blood coagulation disorders), electrolyte imbalance disorders (e.g. hyponatraemia or hyperkalaemia), neoplastic disorders (e.g. nephroma or renal cell cancer) autoimmune diseases, cancers, inflammatory diseases, reproductive system
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diseases, cancers, disorders, endocri:
                                                                                                                 The invention relates to novel nucleic acids and
                                                                                                                                            Claim
                                                                                                                                                                        New polynucleotides and polypeptides, useful for diagnosing, treating, preventing or prognosing e.g. kidney, cardiovascular, blood, electrolyte imbalance or neoplastic disorders, autoimmune diseases,
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28-UUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; neoplastic disease associated polypeptide; cancer; hyperproliferative disorder; neural disorder; immune system disorder muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder;
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14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000;

2000US-0225267. 2000US-0225268. 2000US-0225270. 2000US-0225447.

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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
17-NOV-2000;
17-NO
                                                                                                                                                                                                                                                                                                                                                                          Novel polypeptides and polynucleotides useful as diagnostic reagents diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, and for treating cancers, rheumatoid arthritis -
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11-DEC-2000;
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2000US-0226868 2000US-0227182 2000US-0227182 2000US-0229343 2000US-0229343 2000US-0229343 2000US-0229343 2000US-0229343 2000US-0229343 2000US-022959 2000US-0239437 2000US-0231242 2000US-0231243 2000US-0231414 2000US-0231414 2000US-0231414 2000US-0231414 2000US-0231414 2000US-0231414 2000US-0231414 2000US-0231491 2000US-0232081 2000US-023398 2000US-023398 2000US-023398 2000US-0234201 2000US-0234298 2000US-0234298 2000US-0234298 2000US-023498 2000US-023498 2000US-0235834 2000US-0235834 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836

The present invention relates to the isolation of novel human neoplastic disease associated polypeptides, and cDNA (AAS34767-AAS35050) and DNA CS sequences encoding for these polypeptides. The sequences of the cinvention are useful in the diagnosis, treatment, prevention and/or CC invention are useful in the diagnosis, treatment, prevention and/or CC concer, brain stem glioma, adult liver cancer, childhood cerebellar CC cancer, brain stem glioma, adult liver cancer, childhood cerebellar CC cancer, brain stem glioma, adult liver cancer, childhood cerebellar CC castrocytoma, or Hodgkin's lymphoma). The sequences of the invention may CC also be useful for treating other disorders such as neural disorders, cardiovascular disorders, CC immune system disorders, muscular disorders, reproductive disorders, CC gastrointestinal disorders, muscular disorders, reproductive disorders CC also useful in gene therapy. AAI21568-AAU21851 represent the novel human CC neoplastic disease associated polypeptides of the invention are CC neoplastic disease associated polypeptides of the invention. CC specification, but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published_pct_sequences.

27-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 20-CCT-2000; 02-CCT-2000; 02-CCT-2000; 02-CCT-2000; 02-CCT-2000; 02-CCT-2000; 02-CCT-2000; 02-CCT-2000; 02-CCT-2000; 02-CCT-2000; 03-CCT-2000; 04-NOV-2000; 08-NOV-2000; 08-NOV-2000;

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Copyright (c) 1993 - 2003 Compugen Ltd.
  JC1493
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RESULT 1

S40241

G protein-coupled receptor - great pond snail
C; Species: Lymnaea stagnalis (great pond snail)
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Jun-2001
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Jun-2001
C; Accession: S40241
R; Tensen, C.P.; Kesteren, E.R.; Planta, R.J.; Cox, K.; Burke, J.F.; Heerikhuizen, H.; Vresubmitted to the EMBL Data Library, June 1993
A; Description: A G protein-coupled receptor with LDL-binding motifs suggests a role for 34, A; Accession: S40241
A; Accession: S40241
A; Status: preliminary
A; Molecule type: mRNA
A; Scatus: preliminary
A; Molecule type: mRNA
A; Scatus: preliminary
A; Molecule type: mRNA

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F;118-153/Domain: LDL receptor ligand-binding repeat homology <LDLA>
F;158-194/Domain: LDL receptor ligand-binding repeat homology <LDLB>
F;195-230/Domain: LDL receptor ligand-binding repeat homology <LDLB>
F;233-267/Domain: LDL receptor ligand-binding repeat homology <LDLB>
F;233-267/Domain: LDL receptor ligand-binding repeat homology <LDLC>
F;274-316/Domain: LDL receptor ligand-binding repeat homology <LDLC>
F;367-401/Domain: LDL receptor ligand-binding repeat homology <LDLC>
F;367-401/Domain: LDL receptor ligand-binding repeat homology <LDLD>
F;406-440/Domain: LDL receptor ligand-binding repeat homology <LDLD>
F;406-43/Domain: LDL receptor ligand-binding repeat homology <LDLD>
F;488-523/Domain: LDL receptor ligand-binding repeat homology <LDLD>
F;488-523/Domain: LDL receptor ligand-binding repeat homology <LDLB>
F;508-607/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;508-655/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;508-657/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;704-727/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-1115 <TEN>
A;Cross-references: EMBL:Z23104; NID:g438128; PID:g438129
C;Superfamily: great pond snail LDL receptor-related G protein-coupled receptor; LDL rece
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G protein-coupled receptor - sea anemone (Anthopleura elegantissima)
C;Species: Anthopleura elegantissima
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 21-Jul-2000
C;Accession: JC2033; S41908
C;Nothacker, H.P.; Grimmelikhuijzen, C.J.P.
Biochem: Biophys. Res. Commun. 197, 1062-1069, 1993
A;Title: Molecular cloning of a novel, putative G protein-coupled receptor from sea anem
A;Reference number: JC2033; MUID:94107299; PMID:8280121
A;Accession: JC2033
A;Molecule type: mRNA
A;Residues: 1-925 <NOTY
A;Cross-references: EMBL: Z28332; NID:9452810; PIDN:CAA82186.1; PID:9452811
C;Superfamily: leucine-rich alpha-2-glycoprotein repeat homology <LRR1-F;61-84/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2-F;10-133/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2-F;10-133/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3-F;134-157/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3-F;33-349,350-384,385-419,420-453,454-462/Region: glycine-rich
F;530-551/Domain: transmembrane #status predicted <TM1-F;562-884/Domain: transmembrane #status predicted <TM3-F;500-628/Domain: transmembrane #status predicted <TM3-F;500-628/Domain: transmembrane #status predicted <TM3-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fisher-Fis
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N,Alternate names: follicle stimulating hormone receptor

C,Species: Ovis orientalis aries, Ovis ammon aries (domestic she
C,Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
C,Accession: JC1493; 147080

R;Khan, H.; Yarney, T.A.; Sairam, M.R.
Biochem. Biophys. Res. Commun. 190, 888-894, 1993

Biochem. Biophys. Res. Commun. 190, 888-894, 1993

A;Title: Cloning of alternately spliced mRNA transcripts coding
A;Reference number: JC1493; MUID:93176195; PMID:8439338

A;Accession: JC1493
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C;Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein C;Superfamily: glycoprotein d;Reywords: G protein-coupled receptor; glycoprotein; transmembrane protein F;71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR-F;191,199/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Residues: 1-695 <YAR>
A;Cross-references: GB:L07302; NID:g165884; PIDN:AAA31525.1; PID:g165885
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R;Yarney, T.A.; Sairam, M.R.; Khan, H.; Ravindranath, N.; Payne, S.; Seidah, N.G.
Rol. Cell. Endocrinol. 93, 219-226, 1993
A;Title: Molecular cloning and expression of the ovine testicular follicle stimulating seterence number: I47080; MUID:93351750; PMID:8394255
Cccession: I47080
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#text change 21-Jan-2000
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A; Residues: 1-695 < GRO>
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                      -HNYRQRKSMDSKGIRKHMLHHSSGGKCGHCRRCH
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Ajpescription: receptor that mediates the biochemical effects of follitropin (cjsuperfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat hormone; glycoprotein; hormone receptor; phosphoprotein; f;1-17/Domain: signal sequence #status predicted <SIG> F;18-695/Product: follitropin receptor #status predicted <PFH> F;18-695/Product: follitropin receptor #status predicted <PFH> F;18-695/Product: follitropin receptor #status predicted <PFH> F;18-120/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3> F;56-120/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8> F;121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8> F;172-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8> F;194-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7> F;194-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8> F;194-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9> F;194-2
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A;Title: Molecular cloning of the testicular follicle stimulating hormone receptor of A;Reference number: JN0898; MUID:94071854; PMID:7504463
A;Accession: JN0898
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F;399-421/Domain: transmembrane #status predicted <TM2>
F;444-465/Domain: transmembrane #status predicted <TM3>
F;444-465/Domain: transmembrane #status predicted <TM3>
F;486-508/Domain: transmembrane #status predicted <TM4>
F;529-550/Domain: transmembrane #status predicted <TM5>
F;574-597/Domain: transmembrane #status predicted <TM6>
F;597-630/Domain: transmembrane #status predicted <TM6>
F;609-630/Domain: transmembrane #status predicted <TM6>
F;191-199,293,318/Binding site: phosphate (Tm7) (covalent) (by protein kinase C) #status predicted F;556/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted F;596/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
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A;Note: the authors translated the codon AGT for residue 488 as Arg
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               follitropin receptor precursor - crab-eating macaque
N;Alternate names: follicle-stimulating hormone receptor (FSHR)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JN0898; S36452
R;Gromoll, J.; Dankbar, B.; Sharma, R.S.; Nieschlag, E.
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F;692-712/Domain: transmembrane #status predicted <TM5>
F;740-763/Domain: transmembrane #status predicted <TM6>
F;740-763/Domain: transmembrane #status predicted <TM6>
F;775-795/Domain: transmembrane #status predicted <TM7>
F;61,52,612,435,491,455/Binding site: carbohydrate (Asn) (covalent) #status predicted F;553,645,855,859,868,994,900/Binding site: phosphate (Ser) (covalent) #status predicted F;649,853/Binding site: phosphate (Thr) (covalent) #status predicted
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                                                                                                         TDALCWIPI-FVAKELSLLQVEIPGTITSWVVIGYSAINSALNPILYTLTTRREKE----
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TDFLCMAPISFFAISASLKVPLITVSKAKILLVLFYPINSCANPFLYAIFTKNFRRDFFI
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lutropin-choriogonadotropin receptor precursor (splice form A) - p: N;Alternate names: luteinizing hormone-choriogonadotropin receptor C;Speciles: Sus scrofa domestica (domestic pig) C;Date: 22-dan-1993 #sequence_revision 22-dan-1993 #text_change 21-C;Accession: A41344
C;Accession: A41344
C;Accession: A41344
C;Accession: A41344
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A;Title: Cloning and sequencing of porcine LH-hCG receptor cDNA: variants lacking transm A;Reference number: A41344; MUID:89332517; PMID:2502844
A;Accession: A41344
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A; Reference
A; Contents:
C; Function:
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                                                                                A;Residues: 1-692 <HEC>
A;Cross-references: GB:S81198; NID:g245344; PIDN:AAB21415.1; PID:g245345
A;Cross-references: GB:S81198; NID:g245344; PIDN:AAB21415.1; PID:g245345
A;Cross-references: GB:S81198; NID:g245344; PIDN:AAB21415.1; PID:g245345
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:81117, NCBIN:81119, A;Date of NCBIN:81117, NCBIN:81119, A;Date of NCBIN:81117, NCBIN:81119, NCBIN:8111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOI. Endocrinol. 6, 70-80, 1992
A;Title: Structural organization of the follicle-stimulating hormone receptor A;Reference number: A41729; MUID:92149579; PMID:1738373
A;Accession: A41729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-692 <SPR>
A;Residues: 1-692 <SPR>
A;Cross-references: GB:L02842; NID:g204183; PIDN:AAA41175.1; PID:g204184
R;Heckert, L.L.; Daley, I.J.; Griswold, M.D.
Mol. Endocrinol. 6, 70-80, 1992
                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-692 <H
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A;Accession: A34548
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perfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat
words: alternative splicing; G protein-compled receptor; glycoprotein; membrane pr
jr27/Domain: signal sequence #status predicted <SIG>
j28-696/Broduct: lutropin-choriogonadotropic hormone receptor #status predicted <MAT>
j99-123/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>
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;Residues: 1-696 <LOO>
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Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999

Ccession: A34548; A41729
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Endocrinol. 4, 525-530, 1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The testicular receptor for follicle stimulating hormone: structure and ice number: A34548; MUID:91125358; PMID:2126341
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                                                   annotation;
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                                               glycosylation sites
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F;146-169/Domain: 1
F;172-193/Domain: 1
F;194-218/Domain: 1
F;367-387/Domain: t
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F;191,199,293/Binding site: carbohydrate (ABN) (covalent) #status predicted F;554/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status F;559/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status
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F;71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;96-120/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;146-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;172-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;172-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;194-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Houde, A.; Lambert, A.; Saumande, J.; Silversides, D.W.; Lussier, J.G. Mol. Reprod. Dev. 39, 127-135, 1994
A;Title: Structure of the bovine follicle-stimulating hormone receptor CA;Reference number: I45896; MUID:95127199; PMID:7826612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        follicle stimulating hormone receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 21-Jan-2000
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Best Local S
Matches 43
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les 47; Conserv
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                                                                                                      SQLYVMSL-LVLNVLAFVVICGCYTHIYLTVRNPNITSS-----SSDTKIAKRMAMLIF 579
                                                TDALCWIPI-FVAKPLSLLQVEIPGTITSWVVIGYSAINSALNPILYTLTTRPFKE----
  TDFLCMAPISFFAISASLKVPLITVSKSKILLVLFYPINSCANPFLYAIFTKNFRRDFFI 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-695 <HOU>
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nilarity 27.3%;
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Pred. No. 3.6
                                                                                                                                                                                                                                             Score 139.5;
Pred. No. 3.6
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A; Map position: 3 q2.2-q2.3

C; Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein C; Superfamily: glycoprotein hormone receptor; transmembrane protein C; Keywords: G protein-coupled receptor; hormone binding #status predicted <HOB> F; 11-365/Domain: follicle-stimulating hormone binding #status predicted <HOB> F; 70-94/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR> F; 366-388/Domain: transmembrane #status predicted <TM1> F; 366-388/Domain: transmembrane #status predicted <TM2> F; 443-444/Domain: transmembrane #status predicted <TM3> F; 448-40/Domain: transmembrane #status predicted <TM4> F; 485-507/Domain: transmembrane #status predicted <TM4
A;Introns: 58/2; 82/2; 107/2; 132/2; 157/2; 183/2; 206/2; 231/2; 293/2; 320/2
C;Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein
                                                                                                                                                                                                                                                         R;Aatsinki, J.T.; Pietila, E.M.; Lakkakorpi, J.T.; Rajaniemi, H.J. Mol. Cell. Endocrinol. 84, 127-135, 1992
A;Title: Expression of the LH/CG receptor gene in rat ovarian tiss.
A;Reference number: 157668; MUID:92347604; PMID:1353463
                                                                                    A;Cross-references:
C;Genetics:
                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-700 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Rattus sp. (rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
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xperimental source: ovarian granulosa cells
comment: This receptor belongs to the family
ermatogenesis in male and oogenesis in female.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Remy, J.J.; Lahbib-Mansais, Y.; Yerle, M.; Bozon, V.; Gene 163, 257-261, 1995
A;Title: The porcine follitropin receptor: cDNA cloning, A;Reference number: JC4301; MUID:96011644; PMID:7590277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               uteinizing hormone/chorionic gonadotropin receptor
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene: fshr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQIYSVAIFLGINLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLSKFGCYEMQAQTYRTENLSTAHNIHPRN----GHC
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42; Conservative
                                                                                              GB:S40803; NID:g252163; PIDN:AAB22680.1; PID:g252164
                                                                                                                                                                                                   translated from GB/EMBL/DDBC
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Pred. No. 7.2e-06;
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A;Molecule type: protein
A;Residues: 27-33,'X',35-37,'X',39,'X',41-44 <DUF>
R;RoChe, P.C.; Ryan, R.J.
J. Biol. Chem. 264, 4636-4641, 1989
A;Title: Purification, characterization, and amino-terminal sequence
A;Reference number: A32460; MUID:89174723; PMID:2925659
A;Accession: A33460
A;Molecule type: protein
A;Residues: 27-32,'LX',35-37 <ROC>
A;Introns: 58/2; 82/2; 107/2; 132/2; 157/2; 183/2; 206/2; 231/2; 293/2; 320/2 C;Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; horm F;54-77/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: A61453; MUID:90097014; PMID:2601325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:M26199; NID:g205178; R;Dufau, M.L.; Minegishi, T.; Buczko, E.S.; J. Steroid Biochem. 33, 715-720, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M63918; GB:M63919; GB:M63920; GB:M63921; GB:M63922; R;MCGarland, K.C.; Sprengel, R.; Phillips, H.S.; Koehler, M.; Rosemblit, N. Science 245, 494-499, 1989
A;Title: Lutropin-choriogonadotropin receptor: an unusual member of the G R;Reference number: A41343; MUID:89332512; PMID:2502842
A;Accession: A41343
                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
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A; Residues: 1-700 < MCF >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Note: authors translated the codon CAA for residue 307 as R;T8a1-Morris, C.H.; Buczko, E.; Wang, W.; Xie, X.Z.; Dufau, J. Biol. Chem. 266, 11355-11359, 1991
A;Title: Structural organization of the rat luteinizing horm A;Reference number: A40545; MUID:91250455; PMID:2040640
A;Recession: A40545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
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Pred. No. 1.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIDN:AAA41528.1; PID:g205179 Delgado, C.J.; Zhang, R.
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repeat

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F;103-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;128-152/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;138-177/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;180-201/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;180-201/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;202-226/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;368-389/Domain: transmembrane #status predicted <TM1>
F;400-422/Domain: transmembrane #status predicted <TM3>
F;444-466/Domain: transmembrane #status predicted <TM3>
F;449-511/Domain: transmembrane #status predicted <TM4>
F;550-551/Domain: transmembrane #status predicted <TM6>
F;575-598/Domain: transmembrane #status predicted <TM6>
F;610-631/Domain: transmembrane #status predicted <TM7>
F;610-631/Binding site: palmitate (Cys) (covalent) #status predicted
F;647,648/Binding site: phosphate (Thr) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:M81310; GB:M81318; NID:g198811; PIDN:AAA39432.1; PID:g198812
A;Note: sequence extracted from NCBI backbone (NCBIN:84064, NCBIP:84066)
C;Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat C;Keywords: G protein-coupled receptor; transmembrane protein
F;54-77/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;18-102/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;103-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;128-152/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;153-177/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;180-201/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;180-201/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;180-202-226/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
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N;Alternate names: luteinizing hormone-choriogonadotropin receptor

C;Species: Mus musculus (house mouse)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999

C;Accession: A42395

C;Accession: A42395

R;Gudermann, T.; Birnbaumer, M.; Birnbaumer, L.

R;Gudermann, T.; Birnbaumer, M.; Birnbaumer, L.
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A,Accession: A42395
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Best Local
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                                                                                                              528 SQVYILSILL-LNAVAFVVICACYVRIYFAVQNPELTAP-----NKDTKIAKKWAILIF
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                                                    61
                                                                                                                                                               1 AQIYSVAJFIGINLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVF
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                                                                                                                                                                                                                                                            16.2%; Score 134; DB 2; Length 700; 28.0%; Pred. No. 1.3e-05;
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A;Contents: Thyroid
A;Accession: JC7389
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A; Residues: 1-814 < OBA>
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C;Comment: This receptor, a trans
C;Genetics:
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A; Residues: 1-793 <OBA>
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A; Contents: Thyroid
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         AQIYSVAIFLGINLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVF
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                                                                                               16.0%; Score 132; DB 2; ilarity 27.3%; Pred. No. 2.4e-05; Conservative 28; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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R;Oba, Y.; Hirai, T.; Yoshiura, Y.; Kobayashi, T.; Nagahama, Y.
Biochem. Biophys. Res. Commun. 276, 258-263, 2000
A;Title: Cloning, functional characterization, and expression of thyrotropin receptors in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N,Alternate names: thyrotropin receptor a C;Species: Oncorhynchus sp. (salmon) C;Species: Oncorhynchus sp. (salmon) C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 31-Dec-2000 C;Accession: JC7389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thyroid stimulating hormone receptor b - salmon N;Alternate names: thyrotropin receptor b C;Species: Oncorhynchus sp. (salmon) C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Introns: 6.10/3 C;Keywords: glycoprotein; hormone receptor; thyroid gland; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Oba, Y.; Hirai, T.; Yoshiura, Y.; Kobayashi, T.; Nagahama, Biochem. Biophys. Res. Commun. 276, 258-263, 2000
A;Title: Cloning, functional characterization, and expression
                                                                                                                                                                                 A;Gene: tsh-rb
A;Introns: 584/3
C;Keywords: glycoprotein; hormone receptor; thyroid gland; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Comment: This receptor, a transmembrane protein, which mediates the actions of thyrotro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          624 AQVYIVSVLI-LNILAFLVICACYIKIYCTVHNPHYRSG-----SKDTNIAKRMAVLIF 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AQIYSVAIFLGINLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----EMIHRFWHNYRORKSMDSKGIRKHMLHHSSGGKCGHCRR 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TDFLCMAPISFYAMSAVLDRPLITVSNSKILLVLFYPLNSCANPFLYAIFTKAFRGDVFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.2%; Score 134; DB 2; Length 814; 26.8%; Pred. No. 1.5e-05; tive 32; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                 a transmembrane protein, which medaites
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                                                                 40;
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                                                                                                                              Length 793
                                                                 Indels
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C; Keywords: glycoprotein; hormone receptor; transmembrane protein

F; 56-70/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;96-120/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;161-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;116-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;146-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;172-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;194-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;366-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;384-420/Domain: transmembrane #status predicted <TM2>
F;483-464/Domain: transmembrane #status predicted <TM3>
F;485-507/Domain: transmembrane #status predicted <TM5>
F;573-596/Domain: transmembrane #status predicted <TM6>
F;573-596/Domain: transmembrane #status predicted <TM5>
F;608-629/Domain: transmembrane #status predicted <TM6>
F;608-629/Domain: t
                                                                        C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence revision 16-Feb-1996 #text_change 22-Jun-1999
C;Accession: A36243; B36243; A23728; B36120
R;Minegish, T.; Nakamura, K.; Takakura, Y.; Miyamoto, K.; Hasegawa, Y.; Ibu
                                                                                                                                                                                                                  lutropin-choriogonadotropin receptor precursor - human N;Alternate names: luteinizing hormone-choriogonadotropin receptor N;Contains: lutropin-choriogonadotropin receptor precursor long sp
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: GB:870150; NID:g546896; PIDN:AAB30854.1; PID:g546897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Species: Equus caballus (domestic horse)
;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 13-Aug-1999
;Accession: JC237; JC2370
;Robert, P.; Amsellem, S.; Christophe, S.; Benifla, J.L.; Bellet, D.; Koman, ochem. Biophys. Res. Commun. 201, 201-207, 1994
itle: Cloning and sequencing of the equine testicular follitropin receptor.
Reference number: JC2237; MUID:94256980; PMID:8198575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 MIHRFW-----HNYRQRKSMDSKGIRKHMLHHSSGGKCGHC
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                                                 ; Nakamura, K.; Takakura, Y.; Miyamoto, K.; Hasegawa,
1ys. Res. Commun. 172, 1049-1054, 1990
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                   sequencing
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Pred. No. 2.3e-05;
                   human LH/hCG
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                                                                        Y.; Ibuki,
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A. Molecule type: mRNA
A. Molecule type: mRNA
A. Kolecule type: mRNA
A. Residues: 1-6, 'P', 8-18, 'A', 20-26, 'R', 29-43, 'A', 45, 'A', 47, 'RPS', 52-67, 'S',
A. Residues: GB:M73746; NID:g903745; PIDN:AAA70231.1; PID:g903746
A. Experimental source: thyroid
A. Experimental source: thyroid
R. Zhu, H.; Wang, H.; Ascoli, M.
Mol. Endocrinol. 9, 141-110, 1995
Mol. Endocrinol. 9, 141-110, 1995
                                                                                                                                                                                                                                                                              F;645-699/Domain: carboxyl-terminal propeptide #status predicted <CTP>F;99,174,195,291,299,313/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Note: the exact position of the intron cannot be determined from the experimental C;Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repe C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; hormone F;1-699/Product: lutropin-choriogonadotropin receptor precursor, long splice form #s F;1-266,290-699/Product: lutropin-choriogonadotropin receptor precursor, short splice form the figure of the product o
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A;Experimental source: ovary granulosa and luteal cells; thyroid
A;Bxperimental source: ovary granulosa and luteal cells; thyroid
A;Note: 312-Ser was also found; the authors translated the codon UAC for residue 5
A;Note: mRNA from the thyroid is incompletely processed compared with that from th
R;Frazier, A.L.; Robbins, L.S.; Stork, P.J.; Sprengel, R.; Segaloff, D.L.; Cone, R
Mol. Endocrinol. 4, 1264-1276, 1990
A;Title: Isolation of TSH and LH/CG receptor cDNAs from human thyroid: regulation
A;Reference number: A36120; MUID:91155962; PMID:2293030
A;Accession: B36120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: The lutropin/choriogonadotropin receptor is palmitoylated A;Reference number: A57564; MUID:95295727; PMID:7776964
A;Contents: annotation; mutation analysis of palmitate binding site
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A;Gene: GDB:LHCGR
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A; Residues: 1-123, 'R', 125-311, 'N', 313-699 <JIA>
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A;Tille: Expression of human luteinizing hormone A;Reference number: A23728; MUID:92017881; PMID:1A;Accession: A23728
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A;Accession: A36243
A;Molecule type: mRNA
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P15582 sus scrofa
P20395 rattus norv
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                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002172; LDL_recept InterPro; IPR001611; LRR. InterPro; IPR00172; LRR. Nterm. InterPro; IPR003592; LRR_out. InterPro; IPR003591; LRR_typ.
                                                                                                                                                                       VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
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                                                               576
                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                            61
                                                                                <u>بــ</u>
                                                           AQIYSVAIFLGINLAAFIIIVFSYGSMFYSVHQSAITATBIRNQVKKEMILAKRFFFIVF
WHNYRQRKSMDSKG
                                   TDALCWIPIFVAKPLSLLQVEIPGTITSWVVIGYSAINSALNPILYTLTTRPFKEMIHRF 120
                          TDALCWIPIFVVKFLSLLQVEIPGTITSWVVIFILPINSALNPILYTLTTRPFKEMIHRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ne-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000276; GPCR_Rhodpsn.
IPR002172; LDL_recept_A.
IPR001611; LRR.
                                                                                                                                    757 AA;
                                                                                                                                                                      485
36
127
264
272
325
368
63
                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat;
                                                                                                                                     86992 MW;
                                                                                                       77.2%;
94.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alternative
                                                                                                                                                                                                                       LDL-RECEPTOR CLASS A

LRR 1.

LRR 2.

LRR 3.

LRR 4.

LRR 5.

LRR 6.

LRR 7.

LRR 8.

LRR 10.

LRR 10.

BY SIMILARITY.

N'LINKED (GLCNAC...
                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane; Glycoprotein; Repeat;
                                                                                                         Score 638;
Pred. No. 7.
                                                                                                                                            D\text{->}Y\colon LEADS TO CONSTITUTIVE INCREASE BASAL CAMP.
                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL)
GDNNGWSMQFDKYFASYYKWTSQYPFEAETPECL
(IN ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                            7 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ive splicing.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                 N-LINKED
                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                         4 (POTENTIAL)
                                                                                                                                  8079E8DBF3A3EF21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
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                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                              GLCNAC . . .)
                                                                                                        DB 1;
.2e-51;
                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                6
                                                                                                                 Length 757;
                                                                                                Indels
                                                                                                                                                                             (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
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A Harrison W.R., Boettger-Tong H.L., Bishop C.E., Agoulnik A.I.;
A Harrison W.R., Boettger-Tong H.L., Bishop C.E., Agoulnik A.I.;
A Harrison W.R., Boettger-Tong H.L., Bishop C.E., Agoulnik A.I.;

A Harrison W.R., Boettger-Tong H.L., Bishop C.E., Agoulnik A.I.;

A Harrison W.R., Boettger-Tong H.L., Bishop C.E., Agoulnik A.I.;

A Harrison W.R., Boettger-Tong H.L., Bishop C.E., Agoulnik A.I.;

A Harrison W.R., Boettger-Tong H.L., Bishop C.E., Agoulnik A.I.;

A Harrison W.R., Boettger-Tong H.L., Bishop C.E., Agoulnik A.I.;

A Harrison W.R., Boettger-Tong H.L., Bishop C.E., Agoulnik A.I.;

Bediated by G proteins leading to stimulation of adenylate cyclase consultin-like peptide (INSL3) (By similarity)

C --- SUBCELLULAR LOCATION: Integral membrane protein.

C --- SUBCELLULAR LOCATION: Integral membrane protein.

C --- SUBCELLULAR LOCATION: Integral membrane protein.

C --- SUBCELLULAR DECEST IN LORB seems to be a cause of impaired testicular descent (known as cryptorchidism).

C --- SIMILARITY: CONTAINS 1 LEUL-RECEPTOR CLASS A DOWAIN.

C --- SIMILARITY: CONTAINS 1 LEUL-RECEPTOR CLASS A DOWAIN.

C --- SIMILARITY: CONTAINS 1 LEUCINE-RICH REPEATS (LRR).

C --- SIMILARITY: CONTAINS 1 LEUCINE-RICH REPEATS (LRR).

C --- SIMILARITY: CONTAINS 1 LEUCINE-RICH REPEATS (LRR).
TRANSMEM
DOMAIN
TRANSMEM
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TRANSMEM
DOMAIN
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(291.ZZ5;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Relaxin receptor 2 (Leucine-rich repeat-containing G protein-coupled receptor 8) (G protein-coupled receptor affecting testicular descent)
(G protein-coupled receptor 106).

LGR8 OR GREAT OR GPR106.
                                                                                                                                                                                                                                                                                                     InterPro; IPR002172; LDL_recept, InterPro; IPR001611; LRR. InterPro; IPR000372; LRR_Nterm. InterPro; IPR000372; LRR_Nterm.
                                                                                                                                                                                                                                                                                                                                            EMBL; AF346501; AAL08943.1; -. MGD; MGI:2153463; Gpr106. InterPro; IPR000276; GPCR_Rhodpsn. InterPro; IPR002172; LDL recept_A. InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                        G-protein
                                                                                                                                                                                          PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; PROSITE; PS01209; LDLRA_1; 1. PROSITE; PS50068; LDLRA_2; 1.
                                                                                                                                                                                                                                                                 Pfam; PF00001; 7tm_i; 1.—
Pfam; PF00057; ldl_recept_a; 1.
Pfam; PF00560; LRR; 8.
                                                                                                                  TRANSMEM
                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESDOM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                   SM00013; LRRNT;
                                                                                                                                                                      coupled
400
421
439
460
491
512
                                                                                                                                                    repeat
                                                                                                                                                                        receptor;
 399
420
438
459
490
511
520
                                                                                                                                                                  Transmembrane; Glycoprotein; Repeat;
             2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                           CYTOPLASMIC
2 (POTENTIAL
                                                                                                                                EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                             (POTENTIAL).
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LGR8
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                              15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Relaxin receptor 2 (Leucine-rich repeat-creceptor 8) (G protein-creceptor 8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
RE
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TRANSMEM
Gorlov I.P., Kamat A., Jones E., Lamb D., Truong A., Bog
Bishop C.E., McElreavey K., Agoulnik A.I.;
"Mutations of the GREAT gene cause cryptorchidism.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for relaxin. The activity of this
mediated by G proteins leading to stimulation of ade
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                             Sherwood O.D., Hsueh A.J.W.; "Activation of orphan receptors Science 295:671-674(2002).
                                                                                                                               Heu
                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                     Science 295:671-67
[2]
SEQUENCE FROM N.A.
                                                                                                                                         SEQUENCE FROM N.A., AND MUTAGENESIS MEDLINE=21669315; PubMed=11809971;
                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                     632
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                                                                                                                               S.Y., Nakabayashi K.,
                                                                                                                                                                                                                                                                                                                                                                                            YRQR 127
                                                                                                                                                                                                                                                                                                                                                                                                                  YSVAIFLGINLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVFTDA
                                                                                                                                                                                                                                                                                                                                                                      HRRK
                                                                                                                                                                                                                            OR GREAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YSLGIFLGVNLLAFLVIVISYVTMFCSIHKTALQTAEVRSHIGKEVAVANRFFFIVFSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                      695
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167
192
215
239
263
287
312
335
478
478
318
350
361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Leucine-rich repeat-containing tein-coupled receptor affecting t
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                                                                                                                               Nishi
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N-LINKED
N-LINKED
N-LINKED
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Pred. No. 5.7e-30
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CYTOPLASMIC (POTENTIAL).
LDL-RECEPTOR CLASS A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
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CYTOPLASMIC (
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BY SIMILARITY.
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N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
AF60F635EA1ACE49 CF
                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                             s.,
                                                                                                        by the hormone relaxin.";
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                                                                                                                                                       ဝှု
                                                                                                                             Kumagai J.,
                                                                                                                                                     ASP-647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
                                                                                                                              Kudo M.,
                                                                                                                                                                                                                                     g G protein-coupled
testicular descent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
              this receptor
  adenylate
                                                          Bogatcheva
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    InterPro; IPR000276; (InterPro; IPR002172; InterPro; IPR001611; InterPro; IPR003591; InterPro; IPR003591; InterPro; IPR003591; I
             REPEAT
REPEAT
REPEAT
DISULFID
CARBOHYD
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TRANSMEM
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   CARBOHYD
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   1384594417
1384594417
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  GPCR_Rhodpsn.
LDL_recept_A.
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This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-e
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                 testicular descent (known as cryptorchidism). It is one of the most frequent congenital abnormalities in humans, involving 2-5% of male births. Cryptorchidism is associated with increased risk of infertility and testicular cancer.

SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.

SIMILARITY: CONTAINS 10 LEUCINE-RICH REPEATS (LAR).

CAUTION: It is uncertain whether Met-1 or Met-18 is the initiator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and an increase of cAMP. May also be a receptor insulin-like peptide (INSL3).
SUBCELLULAR LOCATION: Integral membrane protein TISSUE SPECIFICITY: Expressed mainly in the braitestis, thyroid, uterus, peripheral blood cells of DISEASE: Defects in LGR8 seems to be a cause of
                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor for Leydig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  brain kidney, muscle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    impaired
                                                                                                                             restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bone
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                                                                                                                                                                     collaboration
6 outstation -
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Pfam; pF000001; 7tm_1; 1.

Pfam; pF000057; ldl recept_a; 1.

Pfam; pF000507; LRR; 8

PFAM; pF000507; LRR; 8

PRINTS; PR00237; GPCRRHODOPSN.

PRINTS; PR00019; LEURICHPPT.

SWART; SM00199; LEURICHPPT.

SWART; SM00199; LEURICHPPT.

SWART; SM00359; LRR TYP; 10.

PROSITE; PS00237; GPROTEIN RECEP_F1_1; FALSE_NEG.

PROSITE; PS00237; GPROTEIN RECEP_F1_2; 1.

RECSITE; PS01009; LDLRA_1; 1.

RECSITE; PS01008; LDLRA_2; 1.

RECSITE; PS01008; LDLRA_2; 1.

RECSITE; PS01008; LDLRA_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane; Glycoprotein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (P
2 (POTENTIAL).
EXTRACELLULAR
3 (POTENTIAL).
CYTOPLASMIC (P
4 (POTENTIAL).
BY SIMILARITY.
N-LINKED (GLCNA
N-LINKED (GLCNA
                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR
5 (POTENTIAL).
CYTOPLASMIC (P
                                                                                                                                                                                                                                                                               EXTRACELLULAR 7 (POTENTIAL)
                                                                                                                                                                                                                                                               CYTOPLASMIC
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 (GLCNAC.
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   (POTENTIAL)
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RESULT 4
GPCR_LYMST
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Best Local
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PIR; S40241; S
HSSP; Q07954;
                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94255418; PubMed=8197140; Tensen C.P., van Kesteren E.R., Planta R.J., Cox K.J.A., Burke J.F., van Heerikhuizen H., Vreugdenhil E.; van Heerikhuizen H., Vreugdenhil E.; "A G protein-coupled receptor with low density lipoprotein-binding motifs suggests a role for lipoproteins in G-linked signal transduction.";
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MUTAGEN
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
G-protein coupled receptor GRL101 precursor.
Lymnaea stagnalis (Great pond snail).
Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
                                                      InterPro;
                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lymnaeidae; Lymnaea.
NCBI_TaxID=6523;
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                                  InterPro;
                                                                         InterPro;
                                                                                                                    InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C. Natl. Acad. Sci. U.S.A. 91:4816-4820(1994).

FUNCTION: MIGHT DIRECTLY TRANSDUCE SIGNALS CARRIED BY LARGE
EXTRACELLULAR (LIPO) PROTEIN (COMPLEXE) S INTO NEURONAL EVENTS.
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN A SMALL NUMBE
NEURONS MITHIN THE CENTRAL NERVOUS SYSTEM AND TO A LESSER EX
                                                                                                                                                                                                                                                                                                                                                                                   IN THE HEART.

SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED SIMILARITY: CONTAINS 12 LDL-RECEPTOR CLASS A DOMAINS. SIMILARITY: CONTAINS 7 LEUCINE-RICH REPEATS (LRR).
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H-QRKSI 714
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            | IPR000276;
| IPR002172;
| IPR001611;
| IPR000372;
| IPR003592;
| IPR003591;
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    LRR_Nterm.
LRR_out.
LRR_typ.
                                                                         LDL_recept_A.
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N-LINKED (GLCNAC...) (POT)
N-LINKED (GLCNAC...) (POT)
N-Y: LEADS TO CONSTITUTIVE
BASAL CAMP.
7088ECD204C6A6C5 CRC64;
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Pred. No. 1.9e-28;
5; Mismatches 26;
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(GLCNAC. ..) (POTENTIAL).
(GLCNAC. ..) (POTENTIAL).
(GLCNAC. ..) (POTENTIAL).
ADS TO CONSTITUTIVE INCREASE
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            R Pfam; pF00001; 7tm_1; 1.

R Pfam; pF00057; ldl recept_a; 11.

R Pfam; pF00565; LRR; 6.

R Pfam; pF01462; LRRNT; 1.

R PFLNTS; PR00237; GPCRRHODOPSN.

R PRLNTS; PR00261; LDLA; 12.

R PRLNTS; PR00261; LDLA; 12.

R SMART; SM00192; LDLA; 12.

R SMART; SM00192; LRR, 2.

R SMART; SM00370; LRR, 2.

R SMART; SM00370; LRRYT; 1.

R SMART; SM00369; LRR TY; 1.

R SMART; SM00369; LRR TY; 1.

R PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.

R PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

R PROSITE; PS0026; LDLRA_1; 6.

R PROSITE; PS0066; LDLRA_2; 11.

R G_PROTEIN COUPLED RECEP_F1_2; 1.

R PROSITE; PS0066; LDLRA_2; 11.
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          ignal
CYTOPLASMIC (POTENTIAL).

12 X 40 AA APPROXIMATE TANDEM REPEATS SIMILAR TO THE LDI-RECEPTOR CLASS A.

LDI-RECEPTOR CLASS A 2.

LDI-RECEPTOR CLASS A 3.

LDI-RECEPTOR CLASS A 3.

LDI-RECEPTOR CLASS A 4.

LDI-RECEPTOR CLASS A 5.

LDI-RECEPTOR CLASS A 6.

LDI-RECEPTOR CLASS A 6.

LDI-RECEPTOR CLASS A 8.

LDI-RECEPTOR CLASS A 9.

LDI-RECEPTOR CLASS A 10.

LDI-RECEPTOR CLASS A 11.

LDI-RECEPTOR CLASS A 11.

LDI-RECEPTOR CLASS A 11.

LDI-RECEPTOR CLASS A 12.

LRR 1.

LRR 2.

LRR 3.

LRR 4.

LRR 5.

LRR 6.

LRR 6.

LRR 7.

BY SIMILARITY.

BY SIMILARITY.
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5 (POTENTIAL)
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EXTRACELLULAR
7 (POTENTIAL)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
Bovidae; Caprinae; Ovis.

NCBI_TaxID=9940;
[1]
                                                                                                            Yarney T.A., Sair....
Yarney T.A., Sair....
Seidah N.G.;
"Molecular cloning and expression
"Molecular hormone receptor.";
a1.219-226
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSHR SHEEP STANDARD; PRT; 695 AA p35379; Q28573; Q28574; Q9TSI9; 01-JUN-1994 (Rel. 29, Created) 01-JUN-1994 (Rel. 29, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation updat Follicle stimulating hormone receptor precu
                                                                                                                                                                                                                                         SEQUENCE FROM
TISSUE=Testis;
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Yarney T.A., Sairam M.R., Khan H.,
                        STRAIN=Dorset-Leicester-Suffolk 1
MEDLINE=93176195; PubMed=8439338;
                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                         testicular follicle
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                                                                                                                                                                                                  Payne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Follitropin
                                                                                                                                                                                                                                                                                                                                                     Bovoidea;
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         InterPro; IPR000276; GPCR Rhodpsn.
InterPro; IPR000372; LRR.
InterPro; IPR000372; LRR.
InterPro; IPR000372; LRR.
Pfam; PF00001; 7tm 1; 1.
Pfam; PF00560; LRR; 4.
Pfam; PF01462; LRRNT; 1.
Pfam; PF01462; LRRNT; 1.
PFAM; SM00013; LRRNT; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1 2; 1.
PROS
                                                                                                                                                                                                                                      EMBL; L07302; AAA31525.1; --
EMBL; L12766; AAA31523.1; --
EMBL; L12767; AAA31524.1; --
EMBL; L36115; AAK70667.1; --
EMBL; AJ31735; CAA10495.1; --
EMBL; AAT31735; CAA10495.1; --
EMBL; AF090438; AAC61749.1; --
EMBL; AF090438; AAC61749.1; --
EMBL; AF090438; AAC61749.1; --
EMBL; AF090438; AGC61749.1; --
EMBL; AGC617493; AGC61749
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repeat;

Glycoprotein; Signal; at; Alternative splici

splicing

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A Sairam M.R., Subbarayan V.S.R.;

(A Sairam M.R.) Subbarayan V.S.R.;

(A Sairam M.R.) Subbarayan V.S.R.;

(C "Characterization of the 5' flanking receptor gene.";

(C elements of the ovine follitropin receptor gene.";

(L) Mol. Reprod. Dev. 48:480-487(1997).

(L) Mol. Reprod. Dev. 48:480-487(1997).

(C elements of the ovine follicle stimulating hormone. The activate of isoform FSH-R1 is mediated by G proteins which activate of isoform FSH-R1 is mediated by G proteins which activate adamylate cyclase. Isoform FSH-R2 and FSH-R3 also bind FSH, but his does not result in activation of adenylate cyclase. Isoform FSH-R3 may be involved in calcium signaling.

(C FSH-R3 may be involved in calcium signaling.

(C ISOFORMS FSH-R1 and FSH-R2); Cell surface (1soform FSH-R3).

(I SOFORMS FSH-R1 and FSH-R2); Cell surface (1soform FSH-R3).

(I SOFORMS FSH-R3 and FSH-R4; are produced by alternative splicing.

(C elements of the produced by alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM FSH-R3), AND CHARACTE STRAIN=Dorset-Leicester-Suffolk 1; TISSUE=Ovary; MEDLINE=20391225; PubMed=10527886; MEDLINE=20391225; PubMed=10527886; Touyz R.M., Saisma M.M., Touyz R.M., Saisma M.M., Touyz R.M., Saisma Structural features and expression of an alternatector type I receptor for follitropin signaling
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Sairam M.R.;
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                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular cloning, structure, and expression of follitropin receptor with selective alteration that affects signaling function.";
Mol. Reprod. Dev. 48:458-470(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98031017; PubMed=9364442;
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                                                                                                                                                                                                                                                                                   ween the Swiss Institute of Bioinformatics
Buropean Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                                                                          FSH/LSH/TSH SUBFAMILY.
SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS
                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It een the Swiss Institute of Bioinfo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell Biol. Res. Commun.
                                                                                                                                                   an email to license@isb-sib.ch).
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; AAA31523.1; -.
; AAA31524.1; -.
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                                                                                                                                                                                                                                removed.
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                                                                                                                                                                                                                                                        its content
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                                                                                                                                                                                                                                                                                                                                             gh a collaboration -
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RESULT 6
GLHR_ANTEL
ID GLHR_A
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Matches
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                                                          p35409;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable glycoprotein hormone G-protein coupled receptor precursor.
Anthopleura elegantissima (Sea anemone).
Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
Nvnantheae; Actiniidae; Anthopleura.
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=94107299; PubMed=8280121;

Nothacker H.-P., Grimmelikhuijzen C.J.P.;

"Molecular cloning of a novel, putative G

"Molecular anemones structurally related to
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27.2%;
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FSH-R4).

MISSING (IN ISOFORM FSH-R4).

DISRTRIRSLPSYGLENLKKLRAKSTYHLKKLPSLE ->
SPLLHCWAHLQSFFFVVCGQREHISEFGLKSKQHPN (I
ISOFORM FSH-R3).

MISSING (IN ISOFORM FSH-R3).

KFGGCYEVQAQTYRSETSFTAHNEHPRNG -> LHCCTVG
CNHFSSLFVARGNIFLNID (IN ISOFORM FSH-R2).

MISSING (IN ISOFORM FSH-R2).
                                                                                                                                                                                                                                                                                                                                                              32;
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Pred. No. 9.5e
32; Mismatches
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LRR 2.
LRR 3.
LRR 4.
LRR 5.
LRR 5.
LRR 6.
BY SIMILARITY.
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5 (POTENTIAL)
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6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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(GLCNAC...)
(GLCNAC...)
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nes 59;
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               protein-coupled members of the
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(POTENTIAL)
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FSH-R2).
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G-protein coupled recognitions; I
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Pfam; PF00560; LRR; 6.
SMART; SM00370; LRR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrictuse by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; JC2033; JC2033.
InterPro; IPR000276; GPCR Rhodpsn.
InterPro; IPR000832; GPCR secretin.
InterPro; IPR001611; LRR.
InterPro; IPR003592; LRR_out.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z28332; CAA82186.1;
PIR; S41908; S41908.
PIR; JC2033; JC2033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LH/CG receptor family from mammals.";

Biochem. Biophys. Res. Commun. 197:1062-1069(1993).

-I- FUNCTION: PROBABLE RECEPTOR FOR GENCOPROTEIN HORMONE.

-I- SUBCELLULAR LOCATION: Integral membrane protein.

-I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED REFSH/LSH/TSH SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                      CWAPIAFFGLLAAFGOTLLTVTQSKILLVFFFPINSICNPFLYAFFTKAFK
                   CWIPI-FVAKPLSLLQVEIPGTITSWVVIGYSAINSALNPILYTLTTRPFK
                                                                               Similarity
37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                coupled receptor; Transmembrane;
                                                                                                                       Conservative
                                                                                                                                           17.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat.
                                                                              b; Score 143; DB
b; Pred. No. 1.4e
21; Mismatches
                                                                                                                       MW;
                                                                                                                              5 (INCOMPLETE).

N-LINKED (GLCNAC. . .) (POTEN
N-SING (IN SHORT ISOFORM).
                                                                                                                                                                                                                                  CYTOPLASMIC (POT
5 X APPROXIMATE '
1 (INCOMPLETE).
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RESULT 7
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   DR PARTE TO THE PROPERTY OF TH
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InterPro; IPR001611; LRR.
InterPro; IPR00372; LRR Nterm.
Pfam; PF00001; 7tm_1; 1.
Pfam; PF00001; 7tm_1; 1.
Pfam; PF001462; LRRNT; 1.
SMART; SM00013; LRRNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oromoll J., Dankhar B., Sharma R.S., Nieschlag E.;
"Molecular cloning of the testicular follicle stimulating hormone
receptor of the non human primate Macaca fascicularis and
identification of multiple transcripts in the testis.";
Biochem. Biophys. Res. Commun. 196:1066-1072(1993).
-!- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY
OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
16-OCT-2091 (Rel. 40, Last annotation update)
Follicle stimulating hormone receptor precursor
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pROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S36452; S36452.
PIR; JN0898; JN0898.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (Some send an email to license@isb-sib.ch).
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SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED
FSH/LSH/TSH SUBFAMILY.
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01-AUG-1990 (Rel. 15, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Lutropin-choriogonadotropic hormone receptor
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EMBL;
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Loosfelt H., Misrahi M., Atger M.
                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                              use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                  Science 245:525-528(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                        Milgrom E.;
"Cloning and sequencing of porcine LH-hCG receptor cDNA: variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Loosfelt H., Misrahi M., Atger M.,
Jolivet A., Guiochon-Mantel A., Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig)
                                                                                                                                  the European Bioinformatics Institute.
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                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Integral men
ALTERNATIVE PRODUCTS: 4 ISOFORMS;
PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO FAMILY 1 OF
FSH/LSH/TSH SUBFAMILY.
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                  AAA31062.1;
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26.5%;
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BY SIMILARITY.

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r S., Jallal
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                                                                                                            There are no restrictions ong as its content is in
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EMBL; M29528; AAA31065
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PIR; B41344; B41344.
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PIR; C41344; C41344.
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InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR000372; LRR.
InterPro; IPR000372; LRR.
InterPro; IPR000372; LRR.
Pfam; PF00001; 7tm_1; 1.
Pfam; PF00500; LRR; 2.
SMART; SM00013; LRRNT; 1.
PROSITE; PS00237; G PROTEIN_RECEP_F1_2; 1.
G-Protein coupled receptor; Transmembrane; Glycoprotein; Signal;
G-Protein coupled receptor; Transmembrane; Glycoprotein; Signal;
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M29528; AAA31065.1;
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InterPro; IPR000372; LRR.
Pfam; PF000001; 7tm_1; 1.
Pfam; PF00560; LRR.; 3.
Pfam; PF01462; LRRNT; 1.
SWART; SW00013; LRRNT; 1.
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PROSITE; PS50262; G_PROTEIN_RECEP_F1 2; 1.
G_Protein coupled receptor; Transmembrane; Glycoprotein;
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P20395;
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MEDLINE=92149579; PubMed=1738373;

Heckert L.L., Daley I.J., Griswold M.D.;

"Structural organization of the follicle-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91125358; PubMed=2126341;
Sprengel R., Braun T., Nikolics K., Segaloff D.L., Seeburg P.H.;
"The testicular receptor for follicle stimulating hormone: structure and functional expression of cloned cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Bukaryota; Eutheria; Rodentia;
Mammalia; Eutheria; Rodentia;
MCBI_TaxID=10116;
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01-FEB-1991 (Rel. 17, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin
                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                            PhosphoryLation;
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PIR; A41729; A41729.
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-!- SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).
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SUBCELLULAR LOCATION: Integral membrane protein.

TISSUE SPECIFICITY: SERTOLI CELLS AND OVARIAN GRANULOSA CELLS.

SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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Sciurognathi; Muridae; Murinae; Rattus.
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C STRAIN=HOLStein; TISSUE=Ovary, and Testis;

MEDLINE=95127199; PubMed=7826612;

A Houde A., Lambert A., Saumande J., Silversides D.W., Lussier J.G.;

T'Structure of the bovine follicle-stimulating hormone receptor complementary DNA and expression in bovine tissues.";

Mol. Reprod. Dev. 39:127-135(1994).

C-I-SUNCTION: RECEPTOR FOR FOLLICLE STRULATING HORMONE. THE ACTIV.

COPTIS RECEPTOR IS MEDIATED BY GROTEINS WHICH ACTIVATE ADENYLATE CYCLASE.

-I-SUNCLULAR LOCATION: Integral membrane protein.

C-I-SUNLLARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS

PSH/LSH/TSH SUBFAMILY.

-I-SUNLLARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).
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                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
use by non-profit institutions as lon modified and this statement is not remove entities requires a license agreement (S or send an email to license@isb-sib.ch).
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994 (Rel. 29, Last sequence update)
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Pred. No. 2.2e-05;
0; Mismatches 60;
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                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Lutropin-choriogonadotropic hormone receptor
(LSH-R) (Luteinizing hormone receptor).
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Pfam; PF00560; LRR; 4.
Pfam; PF01462; LRRNT; 1.
SMART; SM00013; LRRNT; 1.
Callithrix jacchus (Common marmoset).
Eukaryota; Metazoa; Chordata; Craniata; Ven
Mammalia; Eutheria; Primates; Platyrrhini;
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43; Conservative
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Pred. No. 2.2e-05;
3; Mismatches 59;
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (
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EXTRACELLULAR (POTENTIAL)
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   Vertebrata; Euteleostomi;
ni; Callitrichidae;
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(POTENTIAL)
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Best Local :
                        Matches
                                                                    DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhang F.-P., Rannikko A.S., Manna P.R., Fraser H.M., Huhtaniemi I.T.;

"Cloning and functional expression of the luteinizing hormone
receptor complementary deoxyribonucleic acid from the marmoset monkey
testis: absence of sequences encoding exon 10 in other species.";

Endocrinology 138:2481-2490(1997).

-I- FUNCTION: RECEPTOR FOR LUTROPIN-CHORIOGONADOTROPIC HORMONE.
THE ACTIVATE OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
ACTIVATE ADENYLATE CYCLASE.

-I- SUBCELLULAR LOCATION: Integral membrane protein.

-I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
FSH/LSH/TSH SUBFAMILY.

-SIMILARITY: CONTAINS 5 LEUCINE-RICH REPEATS (LRR).
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REPEAT
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DOMAIN
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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Phosphorylation;
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00001; 7tm 1; 1
Pfam; PF00560; LRR; 2.
SMART; SM00013; LRRNT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000276; GPCR Rhodpsn.
InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR Nterm.
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                                    Similarity
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676
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362
372
393
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75677
                                   16.8%;
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                                                              LRR 1.

LRR 2.

LRR 3.

LRR 4.

LRR 5.

LRR 5.

LRR 5.

LR 6.

LR 6.

LR 6.

LR 6.

LR 7.

BY SIMILARITY.

(POT N-LINKED (GLCWAC. . .) (POT M.)

FB018227641654E1 CRC64;
                                Score 139; DB 1;
Pred. No. 2.4e-05;
                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC
2 (POTENTIAL
                                                                                                                                                                                        CYTOPLASMIC
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (FOTENTIAL)
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                       47;
                                          Length 676;
                       Indels
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RESULT 12
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                                                                                     EMBL; L31966; AAA86933.1; -.
EMBL; AF025377; AAC24981.1; -.
HSSP, P23945; IXUN.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR000372; LRR.
InterPro; IPR000372; LRR, Nterm.
Pfam; PF00001; 7tm_1; 1.
Pfam; PF00001; 7tm_1; 1.
Pfam; PF00001; LRR; 2.
Pfam; PF001462; LRRNT; 1.
SMART; SM00013; LRRNT; 1.
SMART; SM00013; LRRNT; 1.
PROSITE; PS00237; G PROTEIN RECEP F1 2; 1.
 CHAIN
DOMAIN
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DOMAIN
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01-FEB-1996 (Rel. 33, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Follicle stimulating hormone receptor precu
                                                    This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Porcine follicle-stimulating hormone receptor.";
Submitted (SEP-1997) to the EMBL/GenBank/DDEJ debases.
-I-FUNCTION; RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY
OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96011644, PubMed=7590277;
Remy J.J., Lahbib-Mansais Y., Yerle M., Bozon V.,
Pajot E., Grebert D., Salesse R.;
"The porcine follitropin receptor: cDNA cloning, if
expression and chromosomal localization of the ger
Gene 163:257-261(1995).
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la Barbera A.R.;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPL. FSH/LSH/TSH SUBPAMILY. SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).
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387
398
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Cetartiodactyla; Suina; Suidae;
POTENTIAL.

FOLLICLE STIMULATING HORMONE EXTRACELULLAR (POTENTIAL).

1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
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Sus.
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REPEAT
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                                         TISHR MOUSE STANDARD; PRT; 700 AA. 1930730; O1-APR-1993 (Rel. 25, Created) O1-APR-1993 (Rel. 25, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Lutropin-choriogonadotropic hormone receptor (LSH-R) (Luteinizing hormone receptor).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            LHCGR OR LHR.
Mus musculus (Mouse)
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Pred. No. 4.1e-05;
6; Mismatches 62;
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   J. Biol. Cnem. 20/1117/2012
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SEQUENCE OF 1-58 FROM N.A.
MEDIJINE=93093308; PubMed=1459341;
Huhtaniemi I.T., Eskola V., Pakarinen P., Matikainen T.,
"The murine luteinizing hormone and follicle-stimulating
"The muriness transcription initiation sites, putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; S49753; AAB2440
EMBL; M81310; AAA3943
EMBL; M87571; AAA3943
PIR; A42395; A42395.
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Mol. Cell. Endocrinol. 88:55-66(1992).
-I- FUNCTION: RECEPTOR FOR LUTROPIN-CHORIOGONADOTROPIC HORMONE.
THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHI ACTIVATE ADENYLATE CYCLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gudermann T., Birnbaumer M., Birnbaumer L.;
"Evidence for dual coupling of the murine luteinizing hormone receptor to adenylyl cyclase and phosphoinositide breakdown and (mobilization. Studies with the cloned murine luteinizing hormone receptor expressed in L cells.";
J. Biol. Chem. 267:4479-4488 (1992).
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prosite; ps50262; G_protein_recep_f1_2; 1.
G-protein_coupled_receptor; Transmembrane; Glycoprotein;
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InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_
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MGD; MGI:96783; Lhcgr.
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or send an email t
                                                                                                                                                                                                                                                                                                                                             Phosphorylation;
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SIMILARITY: CONTAINS 4 LEUCINE-RICH REPEATS (LRR).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            equires a license agreement (S email to license@isb-sib.ch).
   ; AAB24402.1; -.
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    GPCR_Rhodpsn.
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LRR 1.
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4 (POTENTIAL).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

and Ca2+

Sprengel hormone promoter Ж :

WHICH

RECEPTORS

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial is not removed. Usage by and for commercial agreement (See http://www.isb-sib.ch/announce/

LUTROPIN-CHORIOGONADOTROPIC

Signal;

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Best Local
                                                    MEDULANDA MARKA MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING. STRAIN-Sprague-Dawley, TISSUE-Ovary; MEDLINE-92347604; PubMed=1353463; Aatsinki J.T., Pietila E.M., Lakkakorpi J.T., R"Expression of the LH/CG receptor gene in rat or regulated by an extensive alternative splicing transcript.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=89332512; PubMed=2502842; McFarland K.C., Sprengel R., Phillips H Rosemblit N., Nikolics K., Segaloff D.L. "Lutropin-choriogonadotropin receptor: protein-coupled receptor family."; Science 245:494-499(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSHR RAT STANDARD; PRT; 700 AA. P16235; P70646; Q63807; Q63808; Q63809; O1-APR-1990 (Rel. 14, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Lutropin-chorlogonadotropic hormone receptor (LSH-R) (Luteinizing hormone receptor).
                                                                                                                                           SEQUENCE FROM N.A., AND ALTERNATIVE MEDLINE=91006819; PubMed=1976554; Bernard M.P., Myers R.V., Moyle W.R.
                                                                                                                                                                                                                                                                       MEDLINE=91209270; PubMed=2019252; Koo Y.B., Slaughter R.G., Ji T.H.; "Structure of the luteinizing hormone exons of the coding sequence."; Endocrinology 128:2297-2308(1991).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
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Pred. No. 7e-05;
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EMBL; M26199; J
EMBL; M61212; J
EMBL; M61211; J
EMBL; S40803; J
EMBL; S40787; J
    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Asp383 in the second transmembrane domain of the lutropin receptor is important for high affinity hormone binding and cAMP production.", J. Biol. Chem. 266:14953-14957(1991).

-I- FUNCTION: RECEPTOR FOR LUTROPIN-CHORIOGONADOTROPIC HORMONE.
THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
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"Asp383 ir
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MEDLINE=91060531; PubMed=2174034;

TBai-Morris C.H., Buczko E., Wang W., Dufau

"Intronic nature of the rat luteinizing hor

a soluble receptor subspecies with hormone of the state of the second 
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[6]
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Segaloff D.L., Sprengel R., Nikolics K., Ascoli M.;
"Structure of the lutropin/choriogonadotropin receptor.";
Recent Prog. Horm. Res. 46:261-303(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roche P.C., Ryan R.J.; "Purification, characterization,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUTAGENESIS
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MEDLINE=89174723; PubMed=2925659;
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROFSH/LSH/TSH SUBFAMILY.

SIMILARITY: CONTAINS 7 LEUCINE-RICH REPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTIVATE ADENYLATE CYCLASE.
  S40907;
S40909;
S40918;
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S40918
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  AAA41528 1;
AAA41527 1;
AAA41527 1;
AAA41527 1;
AAB22680 1;
AAB22681 2;
AAB22682 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or for luteinizing h
264:4636-4641(1989)
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                                                                                                                                                                                                                                                                                                                     JOINED.
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mone/human choriogonadotropin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           embrane protein.
L ISOFORMS WHICH D
BY ALTERNATIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dufau
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\$40920; \$40795; \$40798; S40803;

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HSSP; P22888; ILUT.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR000372; LRR_Nterm.
InterPro; IPR000372; LRR_Nterm.
Pfam; PF00001; 7tm 1; 1.
Pfam; PF00001; 7tm 1; 1.
Pfam; PF00560; LRR; 1.
SMART; SM00013; LRRT; 1.
SMART; SM00013; LRNT; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
G_PROTEIN_COUpled_receptor; Transmembrane; Gl.
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  AAB22683 1;
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AAB22683 1;
AAB22683 1;
AAB22683 1;
AAB22683 1;
AAB22684 2;
AAB41529 1;
AAA41529 1;
AAA415
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LRR 5.
LRR 6.
LRR 6.
LRR 7.
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3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                       EXTRACELLULAR 5 (POTENTIAL).
                                                                                                                                                                                                                            6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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RESULT 15
FSHR MOUSE STANDARD; PRT; 692 AA.
ID FSHR MOUSE STANDARD; PRT; 692 AA.
AC P35378; Q9QWV8; Q9D4C2;
DT 01-JUN-1994 (Rel. 29, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Follicle stimulating hormone receptor precursor
       PRESERVE AND PRESE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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                                                   RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/60; TISSUB=Testis;

RX MEDLINE=21085660; PubMed=11217851;

RX MEDLINE=21085660; PubMed=11217851;

RX Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno M., Adachi J., Fukuda S.,

RA Arakawa T., Hara A., Fukunishi Y., Konno S., Yamanaka I.,

RA Arakawa K., Izawa M., Nishi K., Xiyosawa H., Kondo S., Yamanaka I.,

RA Asaito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Saito T., Okazaki Y., Gojobori T., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Basaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Sato K., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Sato K., Sato K., Sato K., Sato K., Sato 
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Matches 34
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STRAIN=129/Sv; TISSUE=Testis;

Tena-Sempere M., Manna P.R., Huhtaniemi I.T.;

Tena-Sempere M., Manna P.R.,
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                                       Wynshaw-Boris A
Hayashizaki Y.;
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Mammalia; Eutheria; Rodentia;
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Pred. No. 7e-05;
1; Mismatches
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                                                                                               n K.-F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequences and promoter activity.";

Mol. Cell. Endocrinol. 88:55-66(1992).

-I- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY
OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sprengel R.;
"The murine luteinizing hormone and follicle-stimulating receptor genes: transcription initiation sites, putative receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 409:685-690(2001).
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TRANSMEM
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EMBL; AK016635; BAB30351.1; -.
EMBL; S49632; AAB24401.1; -.
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00237; GPCRRHODOPSN. SMART; SM00013; LRRNT; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_Nterm.
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SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
FSH/LSH/TSH SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).
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Eskola V., Pakarinen P., Matikainen
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CYTOPLASMIC
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FOLLICLE STIMULATING HORMONE RECEPTOR.

EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL)
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7 (POTENTIAL).
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MBL outstation -
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                                                                                                    AQIYSVAIFLGINLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVF 60
                                           TDFLCMAPILFFAISASLKVPLITVSKAKILLVLFYPINSCANPFLYAIFTKNFRRDFFV 638
                                                                 TDALCWIPI-FVAKPLSLLQVEIPGTITSWVVIGYSALNSALNPILYTLTTRPFKE----
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                                                                                                                                             Similarity
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Search completed: February 3, 2003, 14:21:48 Job time : 22 secs

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Result
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O90xc7 salmo salar
O91949 oncorhynchu
O90663 rana catesb
O8sps8 bos taurus
O91948 oncorhynchu
O11596 homo sapien
O14751 homo sapien
O91887 morone saxa
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13.9	13.9	٠	•		•	14.2	•	14.4	14.4	14.4	14.5	•	14.5	14.5	14.6	14.6	•	٠	14.9	•	15.0	15.1	15.2	15.4	15.5	15.7	15.7	15.7
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ALIGNMENTS

IMINARY; PR MBLrel. 13, Crea MBLrel. 17, Last MBLrel. 173113 iker S.E., Richard iker S.E., Richard iker S.E., Richard iten J.R., Yande gers YH.C., Baxter E.G., yani A., Baxter E.G., yani A., Baxter B.G., yani A	IMINARY; PRT; MBLrel. 13, Created) MBLrel. 13, Last sequence MBLrel. 17, Last annowable A. PubMed=10731132; iker S.E., Holt R.A., Scherer S.E., Holt R.A., Scherer S.E., Holt R.A., Scherer S.E., Li P.W. MS S.E., Richards S., tman J.R., Yandell M. gers YH.C., Blazej Messer YH.C., Blazej LC., Baxter E.G., Helt Yani A., An HJ., Ar U A., Baxendale J., E Os P.V., Berman B.P., han M.R., Bouck J., E os P.V., Berman B.P., han M.R., Butler H., C ley S., Dahlke C., Da lcher A., Deng Z., Ma L.E., Downes M., Duga elian A.E., Garg N.S. F., Gorrell J.H., Gu vey D., Heiman T.J., on K.A., Howland T.J. Netter A., Karpen G.H., Ke T. C., Marten M. S., Ke MBLrel. 13, Last sequence	Kimmel	RA Jalali M.	RA Hostin D.,	RA Harris N.I	RA Glodek A.,	RA Fosler C.,	RA Durbin K.	RA Dodson K.,			RA Borkova D.,	RA Beeson K.Y.,	RA Ballew R.M.,												OC Ephydroide				CG4187.	CG4187				AC Q9VYG0;	ID Q9VYG0
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EQUENCE FROM. SEQUENCE FROM. STRAIN-BERKELEY;

RX MEDIAINE-20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.M., Hoskins R.A., Galle R.F.,

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RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

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RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.I.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfamkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bunck J., Brokstein P., Brottier P.,

Chandra I.,
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A Wang S.-Y., Wassarman D.A., Weinstock G.M., Weinstock
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01-MAR-2002 (TrEMBLrel. 20, L
CG5042 OR CG5046.
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Bukaryota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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InterPro; IPR000276; GPCR Rhodpsn.
InterPro; IPR001091; SecE.

Pfam; PF00001; 7tm1; 1.

PRINTS; PR00237; GPCRRHODDPSN.
PROSITE; PS01067; SECE SEC6IG; UNKNOWN 1.

PROSITE; PS01067; SECE SEC6IG; UNKNOWN 1.
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7; Mismatches 67;
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DR J. PRO02106; AAERNA 113aseII.
DR InterPro; IPR002106, AAERNA 113aseII.
DR Fam; PF00001; 7tm 1; 1.

DR Fam; PF00001; 7tm 1; 1.
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Best Local
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                                                                                                                                                                                      O9DGC5

OPDGC5;

O1-MAR-2001 (TrEMBLrel. 16, C
01-MAR-2001 (TrEMBLrel. 16, L
01-DEC-2001 (TrEMBLrel. 19, L
Gonadotropin receptor II.
TGTH-RII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PÉAM; PF00001; 7tm 1; 1.

PRINTS; PR00237; GFCRRHODOPSN,

PROSITE; PS00237; G PROTEIN RECEP FI 1; 1.

PROSITE; PS00237; G PROTEIN RECEP FI 2; 1.

PROSITE; PS50262; G PROTEIN RECEP FI 2; 1.

G-protein coupled receptor; Glycoprotein; Transmembrant SEQUENCE 359 AA; 40880 MM; 71913BEBD7C9E739 CRC64;
                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroide Cichlidae; Oreochromis.
                                                                                                                                                            Oreochromis niloticus
                          Cichlidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        315
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                                                                                                                                                            (Nile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
                                                                                                                                                            tilapia)
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                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                                                                    sequence update)
                                                                                                                                                        (Tilapia nilotica).
                                                                                                                                                                                                                                                                                                                                                                                  693
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Best Local S
Matches 51
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Q95YI6;
01-DEC-2001
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Oba Y., Hirai T., Yoshiura Y., Yao Z., Nagaham
Oba Y., Hirai T., Yoshiura Y., Yao Z., Nagaham
"Tilapia gonadotropin receptor II.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ
EMBL; AB041763; BAB16107.1; -.
HSSP; P22888; 1LUT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00001; 7tm_1; 1. Pfam; PF00560; LRR; 2.
                                                                                                                                                                                                                                                                                                       Pfam; PF00001; 7cm 1; 1.

Pfam; PF00560; LRR; 14.

SMART; SM00013; LRRNT; 1.

SROSITE; PS00339; AA TRNA LIGASE II 2; UNKNOWN PROSITE; PS00237; G FROTEIN RECEP FI 1; UNKNOWN PROSITE; PS00237; G FROTEIN RECEP F1 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Asterina pectinifera (Starfish).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
Asteroidea; Valvatacea; Valvatida; Asterinidae; Asterina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor.
                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AB061862; BAB68209.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glycoprotein hormone receptor family
pectinifera.";
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"cDNA cloning and functional analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002106; AARRIA ligaseII.
InterPro; IPR000276; GPCR Rhodpsn.
InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_Nterm.
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                                                                                                     AQIYSVAIFLGINLAAFIIIVFSYGSMFYSVHQS-AITATEIRNQVKKEMILAKRFFFIV 59
                                                      FTDALCWIPI ---
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                                                                                                                                                                                                                                                                 1012 AA;
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.6%;
     -FVAKPLSLLQVEIPGTITSWVVIGYSAINSALNPILYTLTTRPFK 114
                                                                                                                                                                                                                                                                 112623 MW;
                                                                                                                                                         17.9%; Score 148; DB 5; 32.9%; Pred. No. 1.7e-06; tive 27; Mismatches 51
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                                                                                                                                                                                                                                                                 52A70E7A88C46E0A CRC64;
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s of a novel memb
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                                                                                                                                                                                                                                                                                                                                           UNKCNOWN 1.
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RESULT
Q95Y17
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           RACCOSSECUTION
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Best Local S
Matches 51
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Q95YI7;
01-DEC-2001
01-DEC-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Asterina pectinifera (Starfish).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
Asteroidea; Valvatacea; Valvatida; Asterinidae; Asterina.
MCBI_TaxID=7594;
O98T85 PRELIMINARY; PRT; 696 AA.

Q98T85;
Q1.-UN-2001 (TrEMBLrel. 17, Created)
O1.-UN-2001 (TrEMBLrel. 17, Last sequence update)
O1.-UN-2002 (TrEMBLrel. 21, Last annotation update)
Lucainizing hormone receptor precursor.

Ictalurus punctatus (Channel catfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
Ictaluridae; Ictalurus.

NCBI TaxID=7998;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Mita M., Hirai T., Oba Y., Yoshikuni M., Nagahama Y.;
"cDNA cloning and functional analysis of a novel member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00001; 7tm 1; 1.

Pfam; PF00560; LRR; 14.

SMART; SM00013; LRRWT; 1.

PROSITE; PS00339; AA TRNA LIGASE II 2; UNKNOWN PROSITE; PS00339; AG FROYEIN RECEP F1 1; UNKNOWN PROSITE; PS00337; G FROYEIN RECEP F1 2; 1.

Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB061861; BAB68208.1; ...
InterPro; IPR002106; AALRNA_ligaseII.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR001611; LRR.
InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR. Nterm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KDCKTIMRSLSNRVFRQR-SM-SRSITLSLGRHPS
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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Q64183;
                           InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_Nterm.
Pfam; PF00001; 7tm 1; 1.
Pfam; PF00560; LRR, 3.
Pfam; PF01462; LRRNT; 1.
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Mol. Endocrinol. 6:70-80(1992).
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MEDLINE=92149579; PubMed=1738373;
Heckert L.L., Daley I.J., Griswol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10118;
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SIGNAL 1
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PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS00732; RIBOSOMAL_S16; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000276; GPCR Rhodpsn.
InterPro; IPR000307; Ribosomal_S16.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODDSN.
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HSSP; P22888; 1LUT
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"Molecular Biology of Channel Catfish Gonadotropin Receptors: 1.
Cloning of a Functional Luteinizing Hormone Receptor and Preovul
Induction of Gene Expression.";
Biol. Reprod. 64:1010-1018 (2001).
EMBL; AF285181; AAK16066.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Structural organization
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L; S81117; AAB21415.2; JOINED
L; S81119; AAB21415.2; JOINED
L; S81121; AAB21415.2; JOINED
L; S81171; AAB21415.2; JOINED
L; S81174; AAB21415.2; JOINED
L; S81178; AAB21415.2; JOINED
L; S81178; AAB21415.2; JOINED
L; S81188; AAB21415.2; JOINED
L; S81188; AAB21415.2; JOINED
L; S81189; AAB21415.2; JOINED
L; S81189; AAB21415.2; JOINED
L; S81194; AAB21415.2; JOINED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
imulating hormone receptor.
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77822 MW;
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Pred. No. 3.3e-06;
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4A1FB19CDE070AB6 CRC64;
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Sciurognathi; Muridae; Murinae; Rattus.
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follicle-stimulating
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Best Local Similarity
Matches 35; Conserv
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative thyrotropin receptor TSHR (Fragment).
Salmo salar (Atlantic salmon).
Salmo salar (Atlantic salmon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
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PROSITE; PS00237; G PROT
PROSITE; PS50262; G PROT
Receptor.
SEQUENCE 688 AA; 7734
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NON TER
SEQUENCE
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PROSITE; PS00237; G PROTEIN_RECEP_F1 1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning and characterization of Atlantic salmon ovarian receptor (TSHR) like cDNA.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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222 R
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                                                                                                                                               TDALCWIPI-----FVAKPLSLLQVEIPGTITSWVVIGYSAINSALNPILYTLTTRPF 113
                                                                                                                                                                                                                                        AQIYSVAIFLGINLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVF
                                                                                                                                                                                                     AQVYIVSVLI-LNILAFLVICTCYMKIYYAVHNPYYCSG-----SKNTNIAKRMAIFIF
                                                                                                      TDFLCMAPISFYAMSPVVDRPL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47;
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                                                                                                                                                                                                                                                                                                              Conservative
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34289
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                                                                                                                                                                                                                                                                                                         Score 138; DB 1:
Pred. No. 5e-06;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 139.5; DB 1
Pred. No. 8.3e-06;
0; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                0E3B8032DAF68470 CRC64;
                                                                                                    - ITVSNSKILLVLFYPLNSCANPFLYAIFTKAF
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RESULT Q91949 ID Q9 AC Q9

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Q9I949; Q9I949;

PRELIMINARY;

PRT;

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Best Local
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                                                                                                                                                                                                                                                 Q9DE63;
Q9DE63;
01-MAR-2001
01-MAR-2001
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Thyrotropin
STSH-RA.
                                                                                                                                                                          Rana catesbeiana (Bull frog).
Bukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Anura; Ne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR001611; LRR.
Pfam; PF00001; 7tm_1; 1.
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MEDLINE=20462948; PubMed=11006115;
MEDLINE=10462948; PubMed=11006115;
Oba Y., Hirai T., Yoshiura Y., Kobayashi T., Nagahama Y.;
Cloning, Functional Characterization, and Expression of Thyrotropin "Cloning, Functional Characterization, and Concorhynchus rhodurus).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oncorhynchus rhodurus (amago).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Protacanthopterygii; Salmoniformes; Salm
            SEQUENCE F
MEDLINE=21
                                                                                         MEDLINE=21065155; PubMed=11120886;
Wang L., Bogerd J., Choi H.S., Seong J.Y.,
Blomenrohr M., Troskie B.E., Millar R.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptors in the Thyroid of Amago Salmon (Oncorh Biochem. Biophys. Res. Commun. 276:258-263(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000
01-OCT-2000
                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                 BFGNRHR-3
                                                                                                                                                                                                                           GnRH receptor-3
                                                                                                                                                                                                                                       01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                  Kwon H.B
                                                                                                                                 TISSUE=BRAIN;
                                                                                                                                                                NCBI_TaxID=8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00237; GPCRRHODOPSN.
                                                Proc.
                                                                      Three distinct types
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                                                                                                                                                                                                                                                                                                                                            LLSKVGLCQRRAQLFR-GQTVSSKG-----
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                                                                                                                                                                                                                                                                                                                                                                     ----EMIHRFWHNYRQRKSMDSKGIRKHMLHHSSGGKCGHCRR
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2 FROM N.A.
=21407809;
Oh D.Y.,
                                                                                                                                                                                                                                                                                                                                                                                            814 AA; 91091 MW;
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                                                                                                                                                                                                                          (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
pr-3 (Type III GnRHR).
                                                Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor
                                              Sci.
PubMed=11517181;
Bogerd J., Choi
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                                              U.S.A.
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15,
21,
                                                                      GnRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32; Mismatches
                                                                                                                                                                            a; Craniata; Vertebrata; Euteleostomi;
Neobatrachia; Ranoidea; Ranidae; Rana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
Choi H.S.,
                                              98:361-366 (2001)
                                                                    receptor characterized
                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No.
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R.S.,
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                                                                                           J.M., Chun
.H., McCann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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 Seong J.Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                814;
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Best Local S
Matches 34
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor.
SEQUENCE
                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-HOLSTEIN; TISSUE-CORPUS LUTEUM;
Kawate N., Tamada H., Inaba T., Sawada T.;
"Molecular cloning of a full-length cDNA encoding bov hormone receptor and its expression in COS-7 cells.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databas
                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Luteinizing hormone receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000276; GPCR_Rhodpsn Pfam; PF00001; 7tm_1; 1. PRINTS; PR00237; GFCRRHODOPSN.
                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                             Q8SPS8;
                                                                                                                                                                                                                                                                                                                                                                                                                             884880
                                                                                                                                                                                  EMBL; AF491303; AAM09535.1; -.
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                                                                                                                                                                                                                                                                                                      Bovidae; Bovinae; Bos.
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                        61
                                                                1 AQIYSVAIFLGINLAAFIIIVFSYGSMEYSVHQSAITATEIRNQVKKEMILAKREFFIVF
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                                                 SQVYILTILI-LNVMAFIIICACYIKIYFAVQNPELMAT-----NKDTKIAKKMAVLIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLFTIHFRREIRRVCRCATQGKDADATSLGTGSFRISTAAVPLKRSAGASGGSCKFDLEV
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 TDFTCMAPISFFAISAAFKVPLITVTNSKVLLVLFYPVNSCANPFLYAIFTKAFQ
                        TDALCWIPI-FVAKPLSLLQVEIPGTITSWVVIGYSAINSALNPILYTLTTRPFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44;
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                                                                                                                  Similarity
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                                                                                                       Conservative
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                                                                                                                                                        ΑA;
                                                                                                                                                        78455 MW;
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                                                                                                                  16.0%;
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                                                                                                       26;
                                                                                                                Score 132; DB 6;
Pred. No. 4.9e-05;
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                                                                                                                                                        D70AE862EB265CCF
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RESULT Q91948

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Best I
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                                                                                                                                                                                                                                                                                                       Luteinizing hormone receptor.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996
01-NOV-1996
01-DEC-2001
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01-OCT-2000
01-OCT-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDILINE=20462948; PubMed=11006115;
Oba Y., Hirai T., Yoshiura Y., Kobayashi T., Nagahama Y.;
Oba Y., Hirai T., Yoshiura Y., Kobayashi T., Nagahama Y.;
Cloning, Functional Characterization, and Expression of Thyrotropin Receptors in the Thyroid of Amago Salmon (Oncorhynchus rhodurus).";
Biochem. Biophys. Res. Commun. 276:258-263(2000).
EMBL; AB030955; BAB07801.1; -.
HSSP; P16473; 1XUM.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR0001611; LRR.
                                                                                                                                          Jia X.C., Oikawa M., Bo M., Tanaka T., Ny "Expression of human luteinizing hormone with LH and chorionic gonadotropin from h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oncorhynchus rhodurus (amago).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID=41164;
                                                                                               ovine species.";
Mol. Endocrinol.
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00001; 7tm 1; 1.

Pfam; PF00560; LRR; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; UNKNOWN 1.

PROSITE; PS50262; G PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                    MEDLINE=92017881; PubMed=1922095;
                                                                                                                                                                                                                                             TISSUE=OVARY;
                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 705
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                      Endocrinol. 5:759-768(1991).

557793; AAB19917.2; -.

P22888; ILUT.

Pro; IPR000276; GPCR_Rhodpsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQVYIISVLI-LNILAFLVICTCYVKIYCAVHNPYYCSG-----SKDTNIAKRMAILIF
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33; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89410 MW;
GPCR_Rhodpsn
LRR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 132; DB 13;
Pred. No. 5.6e-05;
B; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2842BF0D67ED93DC CRC64;
                                                                                                                                          from human
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RESULT
Q14751
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Best Local S
Matches 34
PROSITE; I
Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                           EMBL;
EMBL;
                                                                               Pfam; PF00001; 7tm 1; 1
Pfam; PF00560; LRR; 3.
SMART; SM00013; LRRNT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q14751;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
LUTEINISING hormone-choriogonadotropin receptor (Lu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000372; LRR_Nterm.

Pfam; PF000001; 7tm_1; 1.

Pfam; PF00560; LRR; 3.

SMART; SM00013; LRRNT; 1.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

Receptor.
                                                                                                                                                                                                           HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=96023956; Atger M., Misrahi
                                                         PROSITE;
                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIINE=96023956; PubMed=7556872;
Atger M., Migrahi M., Sar S., Leflem L., Dessen P., Milgrom E.;
"Structure of the human luteinizing hormone-choriogonadotropin
receptor gene: unusual promoter and 5' non-coding regions.";
Mol. Cell. Endocrinol. 111:113-123(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q14751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
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                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Human luteinizing
exon 1 coding regi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-56 FROM N.A. Isai-Morris C.H., Geng Y.,
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                                                                                                                                                                                                    L; X84753; CAA59234.1; JC: X84754; CAA59234.1; JO: L; X84756; CAA59234.1; JO: L; X84757; CAA59234.1; JO: L; X84757; CAA59234.1; JO: L; X84758; CAA59234.1; JO: L; X84758; CAA59234.1; JO: L; X84760; CAA59234.1; JO: L; X84761; CAA59234.1; JO: L; X84761; CAA59234.1; JO: L; X84762; CAA59234.1; JO: L; X84762; CAA59234.1; JO: L; X84762; CAA59234.1; JO: X84762; CAA59234.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coding region
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                                      PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                  IPR000276; GPCR_Rhodpsn
IPR001611; LRR.
                                                                                                                                        IPR000372; LRR_Nterm
  701
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llarity 29.6%;
Conservative 2
  AA;
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78757 MW; E69FFF5BABC409D4 CRC64;
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identical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 131; DB 4;
Pred. No. 6.2e-05;
5; Mismatches 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2E3D93F4621BA842 CRC64;
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M
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gene containing 6 bp
5' flanking sequence
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RESULT 15
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Search completed: February
Job time : 75 secs
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Best Local S
Matches 34
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Q918N7;
01-0CT-2000 (TrEMBLrel. 15, Creat
01-0CT-2000 (TrEMBLrel. 20, Last
01-MAR-2002 (TrEMBLrel. 20, Last
Thyrotropin receptor precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUB-OVARY;

MEDLINB-20457(9); PubMed-11000515;

Kumar R.S., Ijiri S., Kight K., Swanson P., Dittman A., Alok D.,

Zohar Y., Trant J.M.;

"Cloning and functional expression of a thyrotropin receptor from the

gonads of a vertebrate (bony fish); potential thyroid-independent role

for thyrotropin in reproduction.";

Mol. Cell. Endocrinol. 167:1-9(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00237; GPCRRHODOPSN.
PROSTIE; PS00237; GPROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSTIE; PS0262; GPROTEIN_RECEP_F1_2; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
Moronidae; Morone.
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SIGNAL 1
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InterPro; IPR001611; LRR.
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                                                                                                                                                                                                                                                               1 AQIYSVAIFLGINLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVF 60
                                                                                                                                                                                        TDALCWIPI-FVAKPLSLLQVEIPGTITSWVVIGYSAINSALNPILYTLTTRPFK 114
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                                                                                                                               TDFLCMAPISFYAMSAVLDRPLITVSNSKILLVLFYPLNSCANPFLYAIFTKAFR 695
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779 AA; 87400 MW;
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
                        2003, 14:24:43
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Perfect score:
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seq length: 2000000000
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Match
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/FCTUS_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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Gapop 10.0 , Gapext 0.5
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826
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Maximum Match 100%
Listing first 45 summaries
       AQIYSVAIFLGINLAAFIII......HMLHHSSGGKCGHCRRCHLS
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       Length
       3, 2003, 14:19:02 ; Search time 22 Seconds (without alignments) 209.973 Million cell updates/sec
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    US-07-741-453A-56
US-07-757-342D-4
US-07-757-342D-18
US-07-757-342D-18
PCT-US-31-342D-19
US-07-757-342D-19
US-07-757-342D-10
US-07-757-342D-10
US-07-757-342D-10
US-07-757-342D-10
US-07-757-342D-2
US-08-795-876-3
US-08-795-876-3
US-08-487-886-2
US-08-487-886-2
US-08-487-886-2
US-08-487-886-2
US-08-487-95-876-3
US-08-487-986-2
US-08-487-986-2
US-08-487-986-2
US-08-487-986-2
US-08-487-986-2
US-08-487-986-2
US-08-487-988-3
US-08-293-563-5
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Sequence 56, Appli
Sequence 6, Appli
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Sequence 27, Appli
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Sequence 27, Appli
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Sequence 27, Appli
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AQIYSVAIFL-----GINLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRF 55

Query Match 17.9%; Score 147.5; DB 4; Length 792; Best Local Similarity 25.9%; Pred. No. 8.9e-08; Matches 42; Conservative 27; Mismatches 60; Indels 33; Gaps	RESULT 1 Sequence 56, Application US/07741453A Patent No. 6228597 Patent No. 6228597 REPLICANT: INFORMATION: APPLICANT: LIBERT, FREDERIC APPLICANT: UNGORNTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH FITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH FITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES COUNTRY OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: ADDRESSEE: CUSHMAN STREET: 1615 L STREET, N.W. COUNTRY: WASHINGTON, D.C. COUNTRY: APPLICATION DATA: 10. Version #1.25 FILING DATE: 1991015 CURRENT APPLICATION UNMER: 191015 TELEFAN: CONTINE REPARATION: NAME: KOKULIS, PAUL N. REFERENCE/DOCCET NUMBER: 91913/1107/US/ST TELECOMMUNICATION INFORMATION: NAME: KOKULIS, PAUL N. NAME: KOKULIS, PAUL N. REFERENCE/DOCCET NUMBER: 91913/1107/US/ST TELECOMMUNICATION INFORMATION: TELEFAN: (202) 861-3000 TELEFAN:	28 119.5 14.5 517 2 US-09-030-582-10 Sequence 10, App 30 118 14.3 515 1 US-08-194-338-3 Sequence 61, App 31 117.5 14.2 336 1 US-08-118-270-54 Sequence 61, App 32 117.5 14.2 336 5 PCT-US93-08528-54 Sequence 64, App 33 117.5 14.2 513 2 US-09-266-895-21 Sequence 67, App 34 117.5 14.2 513 3 US-09-266-895-21 Sequence 7, App 35 117.5 14.2 515 1 US-08-404-734A-7 Sequence 21, App 36 117.5 14.2 515 1 US-08-406-855A-2 Sequence 21, App 37 117.5 14.2 515 2 US-08-406-855A-2 Sequence 21, App 38 117.5 14.2 515 2 US-08-406-855A-2 Sequence 22, App 40 117.5 14.2 515 3 US-09-206-899-21 Sequence 22, App 41 117.5 14.2 515 4 US-09-206-899-2 Sequence 22, App 42 117.5 14.2 515 4 US-09-688-415-9 Sequence 22, App 43 117.5 14.2 515 4 US-09-688-415-9 Sequence 9, App 44 117.5 14.2 764 4 US-07-757-342D-5 Sequence 9, App 45 117 14.2 332 1 US-08-349-696-23 Sequence 5, App 56 Sequence 5, App 57 Sequence 5, App 58 Sequence 5, App 59 Sequence 5, App 50 Sequence 5, App 50 Sequence 5, App 51 Sequence 5, App 52 Sequence 5, App 53 Sequence 5, App 54 Sequence 5, App 55 Sequence 5, App 56 Sequence 5, App 57 Sequence 5, App 58 Sequence 5, App 59 Sequence 5, App 50 Sequence 5, App 50 Sequence 5, App 51 Seq
4;	SUCH RECEPTORS	Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli

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US-07-757-342D-4
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Patent No. 6218509

GENERAL INFORMATION:
APPLICANT: IGARASHI, Masso
MINEGISHI, Takashi
MAKAMURA, Kazuto
TITLE OF INVENTION: PROTEIN, DNA AND USE
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                   Matches
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TELLEX: 200391 STRE UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION NUMBER: US/07/757,342D
FILING DATE: 10-Sep-1991
CLASSIFICATION: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: BUCKLEY, Linda M.
REGISTRATION NUMBER: 31003
REFERENCE/DOCKET NUMBER: 41226
TELEPHONE: (617)523-34400
TELEPHONE: (617)523-34400
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                                                                                                                                         524 SQVYILTILI-LNVVAFIIICACYIKIYFAVQNPELMAT-----NKDTKIAKKMAVLIF 576
632
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                                                                                                                                                                                                                                  Local Similarity
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ADDRESSEE: DAVID G. CONLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTRPFKEMIHRFWHNYRORKSMDSKGIRKHMLHHSSGGKCGH 150
                                                                                                                                                                       AQIYSVAIFLGINLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVF 60
                                   FWHNYRORKSMDSKGIRKHMLHHSSGGKCGH 150
                                                                                                     TDALCWIPI-FVAKPLSLLQVEIPGTITSWVVIGYSAINSALNPILYTLTTRPFKEMIHR 119
                                                                       TDFTCMAPISFFAISAALKVPLITVTNSKVLLVLFYPVNSCANPFLYAIFTKAFR-----
                                                                                                                                                                                                                   41;
                                                                                                                                                                                                                                                                                                                                          LENGTH: 696 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 130 Water Street
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                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                  17.0%;
 RDFFLLLSKSGCCKH 646
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Pred. No. 4.4e-07;
6; Mismatches 55
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TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID:
US-07-757-342D-6
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Patent No. 6218509
GENERAL INFORMATION
APPLICANT: IGARASHI, Masao
GENERAL INFORMATION:
APPLICANT: PARMENTIER, MARC
APPLICANT: LIBERT, FREDERIC
APPLICANT: DUMONT, JACQUES
APPLICANT: VASSART, GILBERT
ITILE OF INVENTION: POLYPERTI
TITLE OF INVENTION: ACTIVITY,
TITLE OF INVENTION: AND POLYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                        Sequence 55, Application US/07741453A Patent No. 6228597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 200291 STRE UR INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                    579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,342D
FILING DATE: 10-Sep-1991
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                              639 LLSKFGCYEMQAQIYRTETSSATHNFHARKSHCSSAPRVTNSYVLVPLNHSS 690
                                                                                                                                                                                                                                                                                                                                          116 MIHRF-----MIHHSS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   526 SQLYVMAL-LVLNVLAFVVICGCYTHIYLTVRNPTIVSS-----SSDTKIAKRMATLIF 578
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REGISTRATION NUMBER: 31003
REFERENCE/DOCKET NUMBER: 412
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AQIYSVAIFLGINLAAFIIIVFSYGSMFYSYHQSAITATEIRNQVKXEMILAKRFFFIVF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAKAMURA, Kazuto
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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ADDRESSEE: DAVID G. CONLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                           TDALCWIPI-FVAKPLSLLQVEIPGTITSWVVIGYSAINSALNPILYTLTTRPFKE----
                                                                                                                                                                                                                                                                                                                                                                                    TDFLCMAPISFFAISASLKVPLITVSKAKILLVLFYPINSCANPFLYAIFTKNFRRDFFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MINEGISHI,
    GILBERT

POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR

ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS

AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.9%; Score 139.5; DB . 27.3%; Pred. No. 5.6e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takashi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  115
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CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN

WASHINGTON, D.C.

1615 L STREET, N.W.

NUMBER OF SEQUENCES:

62

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                             Sequence 18,
Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/74
PILING DATE: 19911015
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: li
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MEDIUM TYPE: Disk
                                                                                                                                                                              ent No. 2.

NERAL INFORMATION:

APPLICANT: Murphy, Randall B.

APPLICANT: Schuster, David I.

APPLICANT: Schuster, David I.

APPLICANT: SCHUSTER, DAVID INFORMATION: POLYPEPTIDES OF G-COUPLED PROTEIN

POLYPEPTIDES OF G-COUPLED PROTEIN MI
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                            NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 TTRPFKE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           653 AILIFTDFTCMARATHCGPISFFAISAAFKVPLITVTNSKILLVLFYPVNSCANPFLYAI 712
                                                                                                                                                                                                                                                                                                                                                                                                                  773 -- LSTVRATHCGHCQQ 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 HMLHHSSGGKCGHCRR 153
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 FFIVFTDALCWIPIFVAKPLSLLQVE------ PGTITSWVVIGYSAINSALNPILYTL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: AMINO ACID
                                                                                  STREET: 41.
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Local Similarity 21.9%;
es 43; Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH:
                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQVYILSILIRATHCGLNVVAFVVICACYIRIYFAVQNPELTAP-----NKDTKIAKKM 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTKAFQRDRATHCGFLLLLSRFGCCKRRAELYRRKEFSAYTSNCKNGFPGASKPSQATLK 772
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                                                                                                                                                                                                                                                                                                 9, Application US/08118270 5508384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               795 amino acids
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                                                                                                                   E: BROWDY AND NEIMARK
419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/07/741,453A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 137.5; DB 4; Length 795; Pred. No. 1.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91913/1107/US/ST
                                                                                                                         Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64;
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                                                                                                                                                                                                       METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US93-08528-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18, Application PC/TUS9308528 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 202-628-5197
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FILING DATE: 09-SEP-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                   NERAL INFORMATION:

APPLICANT: New York University

APPLICANT: New York University

TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN

TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
                                             FILING DATE: 09-SEP-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                        COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 LFKFSREKKAAKTLGÍVVGWILCWLÞFFIALÞLGSLFSTLKÞÞDAVFKWFWLGY--FNSC 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295 LNPITYPCSSKEFKRAL 311
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REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                       CITY: Washington STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                            STREET:
               NAME: Townsend, Kevin REGISTRATION NUMBER: (
                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                         APPLICATION NUMBER:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39;
                                                                                                                                                                                                                                                                       20004
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                                                                                                                                                                                                                                                                                                                                        419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                           PCT/US93/08528
           34,033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MURPHY=2A
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Pred. No. 6.3e-07
MURPHY=2 PCT
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                                                                                                                                                                                                                                                                                                                                              Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 370;
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TELEPHONE: 202-628-5197

TELEPHONE:

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US-07-757-342D-3
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PCT-US93-08528-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/07757342D Patent No. 6218509
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 16.5%; Score 136; DB 5; Best Local Similarity 28.5%; Pred. No. 6.3e-07; Matches 39; Conservative 24; Mismatches 50
                                                                                                                                           TELEX: 200291 STRE UR INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 LNPILYTLTTRPFKEMI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 LFKFSREKKAAKTLGIVVGWILCWLPFFIALPLGSLFSTLKPPDAVFKWFWLGY--FNSC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 RFFF-----IVFTDALCWIPIFVAKPLSLL--QVEIPGTITSWVVIGYSAINSA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 QIYSVAIFLGINLAAFIIIVFSYGSMFYSV-----HQSAITATEIRNQVKKEMILAK 53
               MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: BUCKLEY, Linda M.
REGISTRATION NUMBER: 31003
REFERENCE/DOCKET NUMBER: 41226
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH:
                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/757,342D

FILING DATE: 10-Sep-1991

CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAKAMURA, KAZULO
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: IGARASHI, Masao
MINEGISHI, Takas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LNPITYPCSSKEFKRAL 311
                                                         TOPOLOGY: linear
                                                                             LENGTH: 700 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                      TELEPHONE: (617)523-3400
                                                                                                                                                                                    TELEFAX: (617)523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             370 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIKE, BRONSTEIN, ROBERTS &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 370;
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                                                                                                                                                                        Query Match 15.9%; Score 131; DB 4; Length 611; Best Local Similarity 29.6%; Pred. No. 4e-06; Matches 34; Conservative 25; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/07757342D Patent No. 6218509
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 16.2%; Score 134; DB 4; Length 700; Best Local Similarity 27.2%; Pred. No. 2.2e-06; Matches 34; Conservative 31; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 200291 STRE UR INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
         489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      528 SQVYILSILI-LNVVAFVVICACYIRIYFAVQNPELTAP----NKDTKIAKKWAILIF 580
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                                                                                                                         1 AQIYSVAIFLGINLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVF 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,342D
FILING DATE: 10-Sep-1991
CLASSIFICATION: -CURLOWN-
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: IGARASHI, Masao
MINEGISHI, Takashi
NAKAMURA, Kazuto
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
                                    TDALCWIPI-FVAKPLSLLQVEIPGTITSWVVIGYSAINSALNPILYTLTTRPFK 114
TDFTCMAPISFFAISAAFKVPLITVINSKVLLVLFYPINSCANPFLYAIFTKTFQ 543
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                                                                                                                                                                                                                                                                                                                           LENGTH: 611 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BUCKLEY, Linda M. REGISTRATION NUMBER: 31003
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COUNTRY: US
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(617)523-6440
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RESULT 10
US-07-757-342D-10
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US-07-757-342D-7
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GENERAL INFORMATION:
                                                                                                                                                                                                        Sequence 10, Application US/07757342D Patent No. 6218509
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 15.9%; Score 131; DB 4; Length 636; Sest Local Similarity 29.6%; Pred. No. 4.2e-06;
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AQIYSVAIFLGINLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVF 60
       APPLICANT: IGARASHI, Masao
MINEGISHI, Takashi
MINEGISHI, Takashi
NAKANURA, KAZULO
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
CUSHMAN
CUSHMAN
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,342D
FILING DATE: 10-Sep-1991
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAMÉ: BUCKLEY, LINDA M.
REGISTRATION NUMBER: 31003
REFERENCE/DOCKET NUMBER: 4
TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: IGARASHI, Masao
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OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: Massachusetts
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TELEFAX: (617)523-6440
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STREET: 130 Water Street
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Patent No. 6218509
GENERAL INFORMATION:
APPLICANT: IGARASHI, Masao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
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TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,342D
FILING DATE: 10-Sep-1991
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BUCKLEY, Linda M.
REGISTRATION NUMBER: 31003
REFERENCE/DOCKET NUMBER: 41226
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEPHONE: (617)523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    552 TDFTCMAPISFFAISAAFKVPLITVINSKVLLVLFYPINSCANPFLYAIFTKTFQ 606
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                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/07/757,342D
FILING DATE: 10-Sep-1991
CLASSIFICATION: CUNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MINEGISHI, Takashi
NAKAMDRA, KAZUTO
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 10
                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TDALCWIPI-FVAKPLSLLQVEIPGTITSWVVIGYSALNSALNPILYTLTTRPFK 114
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                                                                                                                                                                                                                                                                              ZIP:
                                                                                                                                                                                                                                                                                                  CITY: Boston
STATE: Massachusetts
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 674 amino acids
TYPE: amino acid
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NAME: BUCKLEY, Linda M. REGISTRATION NUMBER: 31003
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REFERENCE/DOCKET NUMBER: 41226
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400

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                                                                                                                                                                                          APPLICATION NUMBER: US/08/795, FILING DATE: CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION: NAME: BRAMAN, SUSAN J. REFERENCE/DOCKET NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603
TELECOMMUNICATION INFORMATION: TELEPHONE: 716-263-1636
TELEPHONE: 716-263-1600
INFORMATION FOR SEQ ID NO: 33: SEQUENCE CHARACTERISTICS: LENGTH: 420 amino acids Type: amino acids
                      Query Match
Best Local S
Matches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6403305
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Geras-Raaka, Elizabeth
APPLICANT: Nussenzveig, Daniel R.
TITLE OF INVENTION: COUPLED RECEPTORS
TITLE OF INVENTION: COUPLED RECEPTORS
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Best Local (
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TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                   TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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CITY: Rochester
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LENGTH: 699 amino acids
TYPE: amino acid
TOPOLOGY: linear
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                          43;
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                      h 15.2%; Score 125.5; DB 4;
Similarity 26.1%; Pred. No. 1e-05;
43; Conservative 30; Mismatches 59;
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                                                              Length 420;
                        Indels
                      33;
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	61 TDALCWIPI-FVAKPLSILQVEIPGTITSWVVIGYSAINSALNPILYTLTTRPFK 114	유 첫
	1 AQIYSVAIFLGINLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVF 60 : : ::: :: :: :: :: :: :: ::	유 성
ø.	Query Match 15.2%; Score 125.5; DB 4; Length 423; Best Local Similarity 26.1%; Pred. No. 1e-05; Matches 43; Conservative 30; Mismatches 59; Indels 33; Gaps	2 111 0
	INFORMATION FOR SEQ ID NO: 38: SEQUENCE CHARACTERISTICS: LENGTH: 423 amino acids TYPE: amino acid STRANDEDNESS: not relevant TOPOLOGY: linear MOLECULE TYPE: peptide -08-795-876-38	US-
	CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION: NAME: BRAMAN, SUSAN J. REGISTRATION NUMBER: 34,103 REFERENCE/DOCKET NUMBER: 1,9603/1280 TELECOMMUNICATION INFORMATION: TELEPHONE: 716-263-1636	
	PUTER EDIUM EDIUM OMPUTE PERATI OFTWAR RENT A PPLICA PPLICA	
	R OF SEQUENCES: 44 R OF SEQUENCES: 44 SPONDENCE ADDRESS: RESSEE: NIXON, HARGRAV: EET: Clinton Square, P EET: Rochester TE: New York NTRY: USA	
	US-08-795-876-38 JS-08-795-876-38 Sequence 38, Application US/08795876 Patent No. 6403305 Patent No. 6403305 PAPPLICANT: Gershengorn, Marvin C. APPLICANT: Gershengorn, Marvin C. APPLICANT: Nussenzveig, Daniel R. TITLE OF INVENTION: STRATEGY TO CLONE DRUGS FOR G PROTEIN TITLE OF INVENTION: STRATEGY TO CLONE DRUGS FOR G PROTEIN	S H
	115EMIHRFWHNYRQRKSMDSKGIRKHMLHHSSGGKCGHC 151	, ६ ६
	61 TDALCWIPI-FVAKPLSLLQVBIPGTITSWVVIGYSAINSALNPILYTLTTRPFK 114	용정
	1 AQIYSYAIFLGINLAAFIIIVYSYGSMYSVHOSAITATEIRNOYKKEMILAKKFFFIVF 60 	8 8

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RESULT 15
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APPLICANT: Gershen;
APPLICANT: Geras-R:
APPLICANT: Nussenz
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INFORMATION FOR SEQ ID NO: 2:
                                                      APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT: Schweickhardt, Rene Lynn
APPLICANT: Cheng, Shirley Vui Yen
APPLICANT: Nugent, No. 5744448een Patrice
TITLE OF INVENTION: Human Follicle Stimulating
TITLE OF INVENTION: Hormone Receptor
NUMBER OF SEQUENCES: 2
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LENGTH: 436 amino acids
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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CITY: Rochester
CITY: New York
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ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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APPLICANT: Geras-Raaka, Elizabeth
APPLICANT: Nussenzveig, Daniel R.
TITLE OF INVENTION: STRATEGY TO CLONE
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                                                                                                                                                                                                                                                                                                                                           321
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ZIP: 14603
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REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AQIYSVAIFLGINLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVF 60
                                                                                                                                                                                                                                                                                                    ----EMIHRFWHNYRQRKSMDSKGIRKHMLHHSSGGKCGHC 151
                                                                                                                                                                                                                                                                                                                                                                          TDALCWIPI-FVAKPLSLLQVEIPGTITSWVVIGYSAINSALNPILYTLTTRPFK-----
                                                                                                                                                                                                                                                                                                                                         TDFLCMAPISFFAISASLKVPLITVSKAKILLVLFHPINSCANPFLYAIFTKNFRRDFFI 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43;
                                                                                                                                   INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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                                                                                                             Kelton, Christie Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.2%; Score 125.5; DB 4; Length 436; 26.1%; Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Release #1.0, Version
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TELEFAX: (617) 723-892
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
COMPUTER: IBM P8/2, model 55 SX
OPERATING SYSTEM: MS-DOS version 4.0
SOFTMARE: VAX/VMS Massll via Kermit to IBM MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 723-1300
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/670,085
                                                                                                                                                                                                   FEATURE:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: putative transmembrane region II LOCATION: 382 to 404 IDENTIFICATION METHOD: similarity to other IDENTIFICATION METHOD: protein-coupled rece IDENTIFICATION METHOD: hydrophobic, about 2
IOCATION: 469 to 491 IDENTIFICATION METHOD: IDENTIFICATION METHOD: IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                      NAME/KEY: putative transmembrane region III LOCATION: 427 to 448 IDENTIFICATION METHOD: similarity to other (IDENTIFICATION METHOD: protein-coupled receptions)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: putative transmembrane region I LOCATION: 350 to 370 IDENTIFICATION METHOD: similarity to other IDENTIFICATION METHOD: protein-coupled recommendation of the protein-coupled recommendation of the protein-coupled recommendation of the protein-coupled recommendation of the protein of
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REGISTRATION NUMBER: 2854
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ADDRESSEE: Ares-Serono, Inc.
STREET: Exchange Place, 37th floor
                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                               IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
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NAME/KEY: putative transmembrane region VII
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            GenCore version 5.1.3 (c) 1993 - 2003 Compugen Ltd.
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Sequence 557, App
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/224,455
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 24
LENGTH: 757
TYPE: PRT
ORGANISM: Homo sapiens
09-928-175-24
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URRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR PPLICATION NUMBER: 60/180,628
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR PILING DATE: 2000-06-28
PRIOR PILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR PILING DATE: 2000-07-11
PRIOR PILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
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Patent No. US20020123618A1
GENERAL INFORMATION:
APPLICANT: Paszty, Christopher J.
APPLICANT: Gong, Jianhua
APPLICANT: Daugherty, Betsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 105, Application No. US20 GENERAL INFORMATION
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APPLICANT: Rogers, No. US2002012361BAlma
TITLE OF INVENTION: Leucine-Rich G Proteir
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 00-1229
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TITLE OF INVENTION: Nuc
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                                                       APPLICATION NUMBER: 60/
FILING DATE APPLICATION
              APPLICATION NUMBER: 60/226,868 FILING DATE: 2000-08-22
                                                                                                    FILING DATE: 2000-07-14
                                                                                                                       APPLICATION NUMBER: 60/218,290
                                                                                                                                                            APPLICATION NUMBER: 60/225,447
                                                                                                                                             FILING DATE: 2000-08-14
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94.8%;
                                                                             60/225,757
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Pred. No. 1.1e-61;
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RAPPLICATION NUMBER: 60/229,345

OR FILING DATE: 2000-09-01

OR APPLICATION NUMBER: 60/229,287

OR FILING DATE: 2000-09-01

OR APPLICATION NUMBER: 60/229,513

OR APPLICATION NUMBER: 60/229,513

OR FILING DATE: 2000-09-05
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FILING DATE: 2000-09-01
APPLICATION NUMBER: 60/234,997
FILING DATE: 2000-09-25
APPLICATION NUMBER: 60/229,343
                                                                                                                                APPLICATION NUMBER: 60/237,039
FILING DATE: 2000-10-02
APPLICATION NUMBER: 60/237,038
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                                       FILING DATE: 2000-09-29
APPLICATION NUMBER: 60/236,802
FILING DATE: 2000-10-02
APPLICATION NUMBER: 60/237,037
                                                                                                   FILING DATE: 2000-10-02
APPLICATION NUMBER: 60/236,370
                                                                                                                                                                            FILING DATE: 2000-09-05
APPLICATION NUMBER: 60/236,367
FILING DATE: 2000-09-29
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FILING DATE: 2000-09-08
APPLICATION NUMBER: 60/229,509
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APPLICATION NUMBER:
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APPLICATION NUMBER: 60/225,268
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APPLICATION NUMBER: 60/224,519
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APPLICATION 1
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DATE
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NUMBER: 60/237,040
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OR APPLICATION NUMBER: 60/249,213
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DR FILING DATE: 2000-08-14
DR APPLICATION NUMBER: 60/225,213
DR FILING DATE: 2000-08-14
DR APPLICATION NUMBER: 60/227,182
DR FILING DATE: 2000-08-22
DR APPLICATION NUMBER: 60/225,214
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FILING DATE: 2000-08-14
ADDITE: 2000-08-14
APPLICATION NUMBER: 60/231,244 FILING DATE: 2000-09-08 APPLICATION NUMBER: 60/233,064
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FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,208
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FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/226,681
FILING DATE: 2000-08-22
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APPLICATION NUMBER: 60/235,836
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APPLICATION NUMBER: 60/249,216
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FILING DATE: 2000-11-08
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APPLICATION NUMBER: 60/241,787
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IORGANISM: Homo sapiens
FEATURE:
FEATURE:
NAME/KEY: SITE
LOCATION: (133)
JOTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                               Best Loc
Matches
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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Patent No. US20020090672AJ
                                                                                                                                                                                                                                                                                           SEQ ID NO 557
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Matches 126; Conserv
                                                                                                                               Query Match
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CURRENT APPLICATION NUMBER: US/09/764,853

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult NUMBER OF SEQ ID NOS: 939

SOFTMARE: Patentin Ver. 2.0
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DR APPLICATION NUMBER: 60/233,063

DR FILING DATE: 2000-09-14

DR APPLICATION NUMBER: 60/232,397

DR FILING DATE: 2000-09-14

DR APPLICATION NUMBER: 60/232,399

DR APPLICATION NUMBER: 60/232,399

DR APPLICATION NUMBER: 60/232,399

DR APPLICATION NUMBER: 60/232,399
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FILING DATE: 2000-09-08
APPLICATION NUMBER: 60/233,065
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FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/241,221
FILING DATE: 2000-10-20
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FILING DATE: 2000-09-14
APPLICATION NUMBER: 60/241,808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                  AQIYSVAIFLGINLAAFIIIVESYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVF
TDALCWIPIFVAKPLSLLQVEIPGTITSWVVIGYSAINSALNPILYTLTTRPFKEMIHRF 120
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                              AQIYSVAIFLGINLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVF
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                                                                                                             Similarity
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                                                                                               Conservative
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                                                                                                             Score 632; DB 10;
Pred. No. 8.4e-62;
                                                                                             Pred. No. 8.40
l; Mismatches
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Pred. No. 8.4e-62;
1; Mismatches 7
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                                                                                                                          Length 176;
                                                                                             Indels
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; Sequence 2009, Application US/09764877
; Patent No. US30020147140A1
; GENERAL INFORMATION:
   APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOPTWARE: Patentin Ver. 2.0
EQ ID NO 2009
; LENGTH: 176
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US-09-764-877-2009
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                                  US-09-928-175-21
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Best Local (
                                                                                     PRIOR APPLICATION NUMBER: 60/224,455
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 718
                                                                                                                                                                                                                                                                                                                                                              Patent No. US2002012
GENERAL INFORMATION:
Query Match
                                                                                                                                                                                                  FILE REFERENCE: 00-1229
CURRENT APPLICATION NUMBER: US/09/928,175
CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                       APPLICANT: Daugherty, Betsy
APPLICANT: Rogers, No. US20020123618Alma
TITLE OP INVENTION: Leucine-Rich G Protein Coupled Receptor-8 Molecules and
TITLE OP INVENTION: Uses Thereof
                                                                                                                                                                                                                                                                                           APPLICANT: Paszty, Christ
APPLICANT: Gong, Jianhua
APPLICANT: Daugherty, Be
APPLICANT: Rogers, No. U
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LOCATION: (133)
                                                     ORGANISM: Mus
                                                                          TYPE: PRT
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mes 126; Conserv
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                                                       musculus
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 49.5%;
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Pred. No. 8.4e-62;
1; Mismatches 7;
   Score 409;
   DB 10;
   Length 718;
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-928-175-20
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; Sequence 13, Application US/09928175
; Patent No. US20020123618A1
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APPLICANT: Gong, Jianhua
APPLICANT: Gong, Jianhua
APPLICANT: Daugherty, Betsy
APPLICANT: Rogers, No. US20020123618A1ma
TITLE OF INVENTION: Leucine-Rich G Protein G
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 00-1229
CURRENT APPLICATION NUMBER: US/09/928,175
CURRENT FILLING DATE: 2001-08-10
PRIOR APPLICATION UNMER: 60/224,455
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 42
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APPLICANT: Daugherty, Betsy
APPLICANT: Daugherty, US20020123618Alma
APPLICANT: ROGETS, NO. US20020123618Alma
TITLE OF INVENTION: Leucine-Rich G Protein (
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 00-1229
FILE REFERENCE: 00-1229
CURRENT APPLICATION NUMBER: US/09/928,175
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/224,455
PRIOR FILING DATE: 2000-08-10
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Matches
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Patent No. US20020123618A1
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Matches 73; Conservative 27;
                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Paszty, Christopher J.
APPLICANT: Gong, Jianhua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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nes 73; Conserv
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Pred. No. 1.1e-36;
?7; Mismatches 24;
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7; Mismatches 24;
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                                                                                              RESULT 10
US-09-928-175-8
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US-09-928-175-13
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SOFTWARE: PatentIn Ver. :
SEQ ID NO 13
Sequence 8, Application US/09928175
Patent No. US20020123618A1
GENERAL INFORMATION:
APPLICANT: Paszty, Christopher J.
APPLICANT: Gong, Jianhua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/928,175
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/224,455
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
SEQ ID NO 12
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APPLICANT: Gong, Jianhua
APPLICANT: Daugherty, Betsy
APPLICANT: Daugherty, Betsy
TITLE OF INVENTION: Leucine-Rich G Proteir
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 00-1229
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TYPE: PRT
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)9-928-175-12
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TYPE: PRT
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81 YSLGIFLGVNLLAFLIIVFSYITMFCSIQKTALQTTEVRNCEGREVAVANREFFIVESDA 540
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Local Similarity 59.1%;
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59.1%; Pred. No. 5.7e-35;
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Pred. No. 6.1e-35;
Pre. Mismatches 26;
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LENGTH: 71
TYPE: PRT
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Best Local S
Matches 75
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/224,455
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Paszty, Christo
APPLICANT: Gong, Jianhua
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APPLICANT: Rogers, No. US20020123618A1ma
TITLE OF INVENTION: Leucine-Rich G Protein Coupled Receptor-8 Molecules and
TITLE OF INVENTION: Uses Thereof
TILE REFERENCE: 00-1229
CURRENT APPLICATION NUMBER: US/09/928,175
CURRENT FILING DATE: 2001-08-10
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TITLE OF INVENTION: Leucine-Rich G Protein
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 00-1229
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                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/224,455 PRIOR FILING DATE: 2000-08-10
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                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 42
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                                                                                                       YSLGIFLGVNLLAFLIIVFSYITMFCSIQKTALQTTEVRNCFGREVAVANRFFFIVFSDA
                                                                                                                      YSVAJFLGINLAAFIIIVFSYGSMFYSVHQSAJTATEIRNQVKKEMILAKRFFFIVFTDA
                                      ICWIPVFVVKILSLFRVEIPDIMISWIVIFFLPVNSALNPILYTLTINFFKDKLKQLLHK 672
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Pred. No. 6.2e-35;
""matches 26;
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US-09-928-175-2
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                                          Query Match
Best Local Similarity 59.1
75; Conservative
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
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Patent No. US20020123618A1
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Patent No. US20020123618A1
GENERAL INFORMATION:
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Best Local Similarity
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/224,455
PRIOR FILING DATE: 2000-08-10
                                                                                                                                                                                                                                                                                                                                                       PPLICANT: Paszty, Christopher J.

PPLICANT: Gong, Jianhua
APPLICANT: Daugherty, Betsy
APPLICANT: Rogers, No. US20020123618Alma
TITLE OF INVENTION: Leucine-Rich G Protein Coupled Receptor-8 Molecules
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 00-1229
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EQ ID NO 7
LENGTH: 730
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CURRENT APPLICATION NUMBER: US/09/928,175
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/224,455
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 42
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TITLE OF INVENTION: Leucine-Rich G Protei
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APPLICANT: Gong, Jianhua
APPLICANT: Daugherty, Be
APPLICANT: Rogers, No. U
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4 YSVAIFLGINLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVFTDA 63
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59.1%;
                                                           47.5%; Score 392.5; DB 10; 59.1%; Pred. No. 6.9e-35; ative 25; Mismatches 26;
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Pred. No. 6.6e-35;
5; Mismatches 26
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APPLICANT: Nikolics, Karoly
APPLICANT: McFarland, Keith C.
APPLICANT: Segalo, Deborah L.
APPLICANT: Seeburg, Peter H.
TITLE OF INVENTION: Glycoprotein Hormone Receptor Molecules
FILE REFERENCE: P0576F1C2
CURRENT APPLICATION UNMBER: US/09/877,804
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: US 08/207,814
PRIOR APPLICATION NUMBER: US 08/207,814
PRIOR APPLICATION NUMBER: US 07/781,153
PRIOR FILING DATE: 1994-03-07
PRIOR FILING DATE: 1991-10-31
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APPLICANT: McFarland, Keith C.
APPLICANT: Segalo, Deborah L.
APPLICANT: Seburg, Peter H.
TITLE OF INVENTION: Glycoprotein Hormone Receptor Molecules
FILE REFERENCE: P0576P1C2
CURRENT APPLICATION NUMBER: US/09/877,804
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: US 08/207,814
PRIOR APPLICATION NUMBER: US 08/207,814
PRIOR FILING DATE: 1994-03-07
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PRIOR FILING DATE: 1991-10-31
PRIOR APPLICATION NUMBER: US 07/347,683
PRIOR FILING DATE: 1989-05-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: deduced sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        509 SQLYVMAL-LVLNVLAFVVICGCYTHIYLTVRNPTIVSS-----SSDTKIAKRMATLIF 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            622 LISKFGCYEMQAQIYRTETSSATHNFHARKSHCSSAPRVTNSYVLVPLNHSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 MIHRF-----MHNYRQRKSMDSKGIRKH-----MLHHSS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       709 H-QRKSI 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 YRQRKSM 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   589 YSLGIFLGVNLLAFLIIVFSYITMFCSIQKTALQTTEVRNCFGREVAVANRFFFIVFSDA 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TDALCWIPI-FVAKPLSLLQVEIPGTITSWVVIGYSAINSALNPILYTLTTRPFKE---- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 16.9%; Score 139.5; DB 10; Length 675;
Local Similarity 27.3%; Pred. No. 2.4e-07;
les 47; Conservative 30; Mismatches 60; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 LCWIPIFVAKPLSLLQVEIPGTITSWVVIGYSAINSALNPILYTLTTRPFKEMIHRFWHN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AQIYSVAIFLGINLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TDFLCMAPISFFAISASLKVPLITVSKAKILLVLFYPINSCANPFLYAIFTKNFRRDFFI 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ICWIPVFVVKILSLFRVEIPDTMTSWIVIFFLPVNSALNPILYTLTTNFFKDKLKQLLHK 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     675
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